

SEQUENCE LISTING

<110> Hermanson, Gary J.

<120> Codon-Optimized Polynucleotide-Based Vaccines
Against Bacillus anthracis Infection

<130> 1530.0460002

<150> US 60/409,307

<151> 2002-09-10

<150> US 60/419,089

<151> 2002-10-18

<160> 76

<170> PatentIn version 3.1

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<211> 1788

<212> DNA

<213> Artificial Sequence

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<223> Synthetic coding region for Human TPA/B. anthracis
antigen fusion protein

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<221> CDS

<222> (13)..(1779)

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Gln	Leu	Ser	Gln	Ile	Leu	Ala	Pro	Asn	Asn	Tyr	Tyr	Pro	Ser	Lys	Asn		
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<223> Human TPA/ B. anthracis antigen fusion protein

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Asp Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile
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His Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp
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Ser Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg
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Ile Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala

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Asp Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys
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Arg Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser
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Ile Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp
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Arg Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr
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Phe Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser
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Asn Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr
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<212> DNA

<213> *Bacillus anthracis*

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Thr	Ala	Pro	Ile	Tyr															

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Gln Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro	
435 440 445	
atc gca tta aat gca caa gac gat ttc agt tct act cca att aca atg	3192
Ile Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met	
450 455 460	
aat tac aat caa ttt ctt gag tta gaa aaa acg aaa caa tta aga tta	3240
Asn Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu	
465 470 475	
gat acg gat caa gta tat ggg aat ata gca aca tac aat ttt gaa aat	3288
Asp Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn	
480 485 490 495	
gga aga gtg agg gtg gat aca ggc tcg aac tgg agt gaa gtg tta ccg	3336
Gly Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val Leu Pro	
500 505 510	
caa att caa gaa aca act gca cgt atc att ttt aat gga aaa gat tta	3384
Gln Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu	
515 520 525	
aat ctg gta gaa agg cgg ata gcg gcg gtt aat cct agt gat cca tta	3432
Asn Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp Pro Leu	
530 535 540	
gaa acg act aaa ccg gat atg aca tta aaa gaa gcc ctt aaa ata gca	3480
Glu Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala	
545 550 555	
ttt gga ttt aac gaa ccg aat gga aac tta caa tat caa ggg aaa gac	3528
Phe Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp	
560 565 570 575	
ata acc gaa ttt gat ttt aat ttc gat caa caa aca tct caa aat atc	3576
Ile Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile	
580 585 590	
aag aat cag tta gcg gaa tta aac gca act aac ata tat act gta tta	3624
Lys Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu	
595 600 605	
gat aaa atc aaa tta aat gca aaa atg aat att tta ata aga gat aaa	3672
Asp Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys	
610 615 620	
cgt ttt cat tat gat aga aat aac ata gca gtt ggg gcg gat gag tca	3720
Arg Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser	
625 630 635	
gta gtt aag gag gct cat aga gaa gta att aat tcg tca aca gag gga	3768
Val Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly	
640 645 650 655	
tta ttg tta aat att gat aag gat ata aga aaa ata tta tca ggt tat	3816
Leu Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr	
660 665 670	
att gta gaa att gaa gat act gaa ggg ctt aaa gaa gtt ata aat gac	3864
Ile Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp	

675	680	685	
aga tat gat atg ttg aat att tct agt tta cgg caa gat gga aaa aca			3912
Arg Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr			
690	695	700	
ttt ata gat ttt aaa aaa tat aat gat aaa tta ccg tta tat ata agt			3960
Phe Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser			
705	710	715	
aat ccc aat tat aag gta aat gta tat gct gtt act aaa gaa aac act			4008
Asn Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr			
720	725	730	735
att att aat cct agt gag aat ggg gat act agt acc aac ggg atc aag			4056
Ile Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys			
740	745	750	
aaa att tta atc ttt tct aaa aaa ggc tat gag ata gga taa			4098
Lys Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly			
755	760		
ggtaattcta ggtgattttt aaattatcta aaaaacagta aaattaaaac atactctttt			4158
tgtaagaaat acaaggagag tatgttttaa acagtaatct aaatcatcat aatcctttga			4218
gattgtttgt aggatcc			4235

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<211> 764

<212> PRT

<213> Bacillus anthracis

<400> 4

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20 25 30	
Gln Glu Asn Arg Leu Leu Asn Glu Ser Glu Ser Ser Ser Gln Gly Leu	
35 40 45	
Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro Met Val Val	
50 55 60	
Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu	
65 70 75 80	
Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly	

85										90					95						
Phe	Ile	Lys	Val	Lys	Lys	Ser	Asp	Glu	Tyr	Thr	Phe	Ala	Thr	Ser	Ala						
			100					105					110								
Asp	Asn	His	Val	Thr	Met	Trp	Val	Asp	Asp	Gln	Glu	Val	Ile	Asn	Lys						
		115					120					125									
Ala	Ser	Asn	Ser	Asn	Lys	Ile	Arg	Leu	Glu	Lys	Gly	Arg	Leu	Tyr	Gln						
	130					135					140										
Ile	Lys	Ile	Gln	Tyr	Gln	Arg	Glu	Asn	Pro	Thr	Glu	Lys	Gly	Leu	Asp						
145					150					155					160						
Phe	Lys	Leu	Tyr	Trp	Thr	Asp	Ser	Gln	Asn	Lys	Lys	Glu	Val	Ile	Ser						
				165					170					175							
Ser	Asp	Asn	Leu	Gln	Leu	Pro	Glu	Leu	Lys	Gln	Lys	Ser	Ser	Asn	Ser						
			180					185					190								
Arg	Lys	Lys	Arg	Ser	Thr	Ser	Ala	Gly	Pro	Thr	Val	Pro	Asp	Arg	Asp						
		195					200					205									
Asn	Asp	Gly	Ile	Pro	Asp	Ser	Leu	Glu	Val	Glu	Gly	Tyr	Thr	Val	Asp						
	210					215					220										
Val	Lys	Asn	Lys	Arg	Thr	Phe	Leu	Ser	Pro	Trp	Ile	Ser	Asn	Ile	His						
225					230					235					240						
Glu	Lys	Lys	Gly	Leu	Thr	Lys	Tyr	Lys	Ser	Ser	Pro	Glu	Lys	Trp	Ser						
				245					250					255							
Thr	Ala	Ser	Asp	Pro	Tyr	Ser	Asp	Phe	Glu	Lys	Val	Thr	Gly	Arg	Ile						
			260					265					270								
Asp	Lys	Asn	Val	Ser	Pro	Glu	Ala	Arg	His	Pro	Leu	Val	Ala	Ala	Tyr						
		275					280					285									
Pro	Ile	Val	His	Val	Asp	Met	Glu	Asn	Ile	Ile	Leu	Ser	Lys	Asn	Glu						
	290					295					300										
Asp	Gln	Ser	Thr	Gln	Asn	Thr	Asp	Ser	Glu	Thr	Arg	Thr	Ile	Ser	Lys						
305					310					315					320						
Asn	Thr	Ser	Thr	Ser	Arg	Thr	His	Thr	Ser	Glu	Val	His	Gly	Asn	Ala						
				325					330					335							

Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val Ser Ala Gly
340 345 350

Phe Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp His Ser Leu Ser
355 360 365

Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr Ala
370 375 380

Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly Thr
385 390 395 400

Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly Lys
405 410 415

Asn Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn Gln Leu Ser Gln
420 425 430

Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro Ile
435 440 445

Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met Asn
450 455 460

Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu Asp
465 470 475 480

Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn Gly
485 490 495

Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val Leu Pro Gln
500 505 510

Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu Asn
515 520 525

Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp Pro Leu Glu
530 535 540

Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala Phe
545 550 555 560

Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp Ile
565 570 575

Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile Lys
580 585 590

Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu Asp
595 600 605

Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys Arg
610 615 620

Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser Val
625 630 635 640

Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly Leu
645 650 655

Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr Ile
660 665 670

Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp Arg
675 680 685

Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr Phe
690 695 700

Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser Asn
705 710 715 720

Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile
725 730 735

Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys Lys
740 745 750

Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly
755 760

<210> 5

<211> 1782

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic coding region for Human TPA/synthetic
antigen fusion protein

<220>

<221> CDS

<222> (13)..(1773)

<223>

<400> 5

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ctg tgt gga gca gtc ttc gtt tcg ccc agc agc gct ggg cca act gtg	99
Leu Cys Gly Ala Val Phe Val Ser Pro Ser Ser Ala Gly Pro Thr Val	
15 20 25	
ccc gac aga gac aat gat gga atc cct gat agt cta gag gtt gag gga	147
Pro Asp Arg Asp Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly	
30 35 40 45	
tac acg gta gat gtc aag aac aaa agg act ttt ctc tcg cct tgg atc	195
Tyr Thr Val Asp Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile	
50 55 60	
tca aat atc cat gag aag aag ggg ctt acc aag tac aag tcc tcc ccc	243
Ser Asn Ile His Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro	
65 70 75	
gag aag tgg tct acc gct tcc gat cca tat agc gat ttc gag aag gtc	291
Glu Lys Trp Ser Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val	
80 85 90	
aca ggc cgg atc gat aaa aat gtg tct cca gag gct aga cac ccc ctg	339
Thr Gly Arg Ile Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu	
95 100 105	
gta gca gcc tac ccg att gta cac gtg gac atg gag aac atc att cta	387
Val Ala Ala Tyr Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu	
110 115 120 125	
agc aaa aac gag gac cag tcc aca caa aac act gac tcc gag acc cgc	435
Ser Lys Asn Glu Asp Gln Ser Thr Gln Asn Thr Asp Ser Glu Thr Arg	
130 135 140	
acc ata tct aaa aac acc agt act tca agg acc cac acc tct gaa gtg	483
Thr Ile Ser Lys Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val	
145 150 155	
cac ggc aat gcg gaa gtc cat gca tcg gat att ggt ggc tcc gtg tca	531
His Gly Asn Ala Glu Val His Ala Ser Asp Ile Gly Gly Ser Val Ser	
160 165 170	
gcc ggc ttt agc aat agc aac tcc tcg acg gtt gcc att gac cac tca	579
Ala Gly Phe Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp His Ser	
175 180 185	
ctg tca tta gca ggt gag agg act tgg gct gaa act atg ggt ctg aat	627
Leu Ser Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn	
190 195 200 205	
acc gcc gat acg gcc cgg ctc aac gca aat att cgg tac gtc aac aca	675

Thr	Ala	Asp	Thr	Ala	Arg	Leu	Asn	Ala	Asn	Ile	Arg	Tyr	Val	Asn	Thr		
				210					215					220			
ggg	act	gct	cct	ata	tat	aac	gtg	ctg	cct	acg	aca	agt	ctt	gtc	ctg		723
Gly	Thr	Ala	Pro	Ile	Tyr	Asn	Val	Leu	Pro	Thr	Thr	Ser	Leu	Val	Leu		
			225					230					235				
ggc	aaa	aat	cag	acc	ctc	gca	acc	att	aag	gca	aag	gaa	aat	cag	ctg		771
Gly	Lys	Asn	Gln	Thr	Leu	Ala	Thr	Ile	Lys	Ala	Lys	Glu	Asn	Gln	Leu		
		240					245					250					
agc	cag	atc	ctc	gcc	cct	aac	aac	tat	tat	cca	tcc	aaa	aat	tta	gcc		819
Ser	Gln	Ile	Leu	Ala	Pro	Asn	Asn	Tyr	Tyr	Pro	Ser	Lys	Asn	Leu	Ala		
	255					260				265							
ccc	ata	gcc	ctg	aac	gcc	cag	gac	gac	ttt	tcc	tct	acc	ccc	ata	act		867
Pro	Ile	Ala	Leu	Asn	Ala	Gln	Asp	Asp	Phe	Ser	Ser	Thr	Pro	Ile	Thr		
270				275					280						285		
atg	aat	tac	aat	cag	ttc	ctg	gag	ctg	gaa	aag	acg	aag	cag	ctg	aga		915
Met	Asn	Tyr	Asn	Gln	Phe	Leu	Glu	Leu	Glu	Lys	Thr	Lys	Gln	Leu	Arg		
				290				295						300			
cta	gac	acc	gat	cag	gtg	tat	gga	aac	ata	gcg	aca	tat	aac	ttt	gag		963
Leu	Asp	Thr	Asp	Gln	Val	Tyr	Gly	Asn	Ile	Ala	Thr	Tyr	Asn	Phe	Glu		
			305					310					315				
aac	ggc	cgc	gtg	cgc	gtc	gac	act	ggg	tca	aac	tgg	tct	gaa	gtt	ctg		1011
Asn	Gly	Arg	Val	Arg	Val	Asp	Thr	Gly	Ser	Asn	Trp	Ser	Glu	Val	Leu		
		320				325						330					
ccg	caa	att	caa	gag	aca	acc	gcc	aga	att	atc	ttt	aat	ggg	aag	gac		1059
Pro	Gln	Ile	Gln	Glu	Thr	Thr	Ala	Arg	Ile	Ile	Phe	Asn	Gly	Lys	Asp		
	335					340					345						
ttg	aac	ctt	gtc	gaa	cgt	aga	att	gcc	gcc	gtg	aac	ccc	agt	gat	cca		1107
Leu	Asn	Leu	Val	Glu	Arg	Arg	Ile	Ala	Ala	Val	Asn	Pro	Ser	Asp	Pro		
350				355						360					365		
ctc	gag	acg	act	aaa	ccg	gat	atg	aca	ctg	aaa	gag	gct	ctg	aag	att		1155
Leu	Glu	Thr	Thr	Lys	Pro	Asp	Met	Thr	Leu	Lys	Glu	Ala	Leu	Lys	Ile		
				370					375					380			
gcc	ttc	gga	ttc	aac	gaa	cct	aat	ggc	aat	ttg	cag	tat	cag	ggg	aaa		1203
Ala	Phe	Gly	Phe	Asn	Glu	Pro	Asn	Gly	Asn	Leu	Gln	Tyr	Gln	Gly	Lys		
			385					390					395				
gac	atc	aca	gag	ttt	gat	ttc	aat	ttc	gat	cag	cag	act	tcc	caa	aat		1251
Asp	Ile	Thr	Glu	Phe	Asp	Phe	Asn	Phe	Asp	Gln	Gln	Thr	Ser	Gln	Asn		
		400					405					410					
atc	aaa	aat	cag	ttg	gca	gag	ctg	aat	gcc	acc	aat	atc	tac	acg	gtt		1299
Ile	Lys	Asn	Gln	Leu	Ala	Glu	Leu	Asn	Ala	Thr	Asn	Ile	Tyr	Thr	Val		
	415					420				425							
ctc	gat	aaa	atc	aaa	ctt	aac	gcc	aag	atg	aac	ata	ttg	att	cga	gac		1347
Leu	Asp	Lys	Ile	Lys	Leu	Asn	Ala	Lys	Met	Asn	Ile	Leu	Ile	Arg	Asp		
430					435				440						445		
aaa	cgc	ttc	cac	tac	gac	cgc	aac	aat	ata	gcc	gta	ggc	gct	gat	gag		1395
Lys	Arg	Phe	His	Tyr	Asp	Arg	Asn	Asn	Ile	Ala	Val	Gly	Ala	Asp	Glu		
				450					455					460			

tct gtc gtc aag gag gct cat agg gaa gtt atc aac agc agt act gaa	1443
Ser Val Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu	
465 470 475	
ggg ctg tta ctt aat atc gac aag gac att cgg aag atc ctg tcc ggg	1491
Gly Leu Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly	
480 485 490	
tat atc gtg gag atc gag gat acc gag ggc ctg aag gaa gtc att aac	1539
Tyr Ile Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn	
495 500 505	
gac cgc tat gat atg ctg aac att tcc agc tta cga cag gac ggt aag	1587
Asp Arg Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys	
510 515 520 525	
aca ttt att gac ttt aaa aag tat aac gac aag cta ccc ctg tac att	1635
Thr Phe Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile	
530 535 540	
tcc aac cca aat tac aaa gtt aat gtg tat gct gta acc aag gag aac	1683
Ser Asn Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn	
545 550 555	
aca atc atc aat cca agc gag aac ggc gat acc agc aca aat gga atc	1731
Thr Ile Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile	
560 565 570	
aaa aag atc ctt ata ttt agt aaa aaa ggc tac gag atc ggt tgaggatcc	1782
Lys Lys Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly	
575 580 585	

<210> 6

<211> 587

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TPA/synthetic antigen fusion protein

<400> 6

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
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Ala Val Phe Val Ser Pro Ser Ser Ala Gly Pro Thr Val Pro Asp Arg
20 25 30

Asp Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val
35 40 45

Asp Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile

50		55		60
His Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp				
65		70	75	80
Ser Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg				
	85	90		95
Ile Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala				
	100	105		110
Tyr Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn				
	115	120		125
Glu Asp Gln Ser Thr Gln Asn Thr Asp Ser Glu Thr Arg Thr Ile Ser				
	130	135		140
Lys Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His Gly Asn				
	145	150	155	160
Ala Glu Val His Ala Ser Asp Ile Gly Gly Ser Val Ser Ala Gly Phe				
	165	170		175
Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp His Ser Leu Ser Leu				
	180	185		190
Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr Ala Asp				
	195	200		205
Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly Thr Ala				
	210	215		220
Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly Lys Asn				
	225	230	235	240
Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn Gln Leu Ser Gln Ile				
	245	250		255
Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro Ile Ala				
	260	265		270
Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met Asn Tyr				
	275	280		285
Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu Asp Thr				
	290	295	300	

Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn Gly Arg
305 310 315 320

Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val Leu Pro Gln Ile
325 330 335

Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu Asn Leu
340 345 350

Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp Pro Leu Glu Thr
355 360 365

Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala Phe Gly
370 375 380

Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp Ile Thr
385 390 395 400

Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile Lys Asn
405 410 415

Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu Asp Lys
420 425 430

Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys Arg Phe
435 440 445

His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser Val Val
450 455 460

Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly Leu Leu
465 470 475 480

Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr Ile Val
485 490 495

Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp Arg Tyr
500 505 510

Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr Phe Ile
515 520 525

Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser Asn Pro
530 535 540

Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile Ile
545 550 555 560

Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys Lys Ile
 565 570 575

Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly
 580 585

<210> 7

<211> 2277

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic coding region for Human TPA/synthetic
 antigen fusion protein

<220>

<221> CDS

<222> (13)..(2268)

<223>

<400> 7

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ctg tgt gga gca gtc ttc gtt tcg ccc agc gaa gtg aag caa gaa aat	99
Leu Cys Gly Ala Val Phe Val Ser Pro Ser Glu Val Lys Gln Glu Asn	
15 20 25	
cga ctt ctg aac gag agc gaa agt tca tca cag ggt ctt ctc gga tac	147
Arg Leu Leu Asn Glu Ser Glu Ser Ser Ser Gln Gly Leu Leu Gly Tyr	
30 35 40 45	
tac ttc agt gac ttg aat ttc caa gca cca atg gtg gtg act agt agc	195
Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro Met Val Val Thr Ser Ser	
50 55 60	
acc acc ggc gat ttg agc att ccc agc tct gag ttg gag aac att ccc	243
Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu Asn Ile Pro	
65 70 75	
agc gaa aat cag tac ttc cag tct gct atc tgg tcc gga ttc att aag	291
Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly Phe Ile Lys	
80 85 90	
gtt aaa aag tcc gac gaa tat aca ttt gct acc tcg gcg gat aac cat	339
Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala Asp Asn His	
95 100 105	

gtg	aca	atg	tgg	gtg	gac	gac	cag	gaa	gtg	atc	aac	aag	gct	tca	aac	387
Val	Thr	Met	Trp	Val	Asp	Asp	Gln	Glu	Val	Ile	Asn	Lys	Ala	Ser	Asn	
110					115					120					125	
tct	aat	aaa	atc	cgg	ctc	gag	aag	ggg	agg	ctc	tac	cag	atc	aaa	att	435
Ser	Asn	Lys	Ile	Arg	Leu	Glu	Lys	Gly	Arg	Leu	Tyr	Gln	Ile	Lys	Ile	
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cag	tac	cag	cgg	gaa	aac	cct	aca	gaa	aaa	gga	ctc	gat	ttc	aag	ctg	483
Gln	Tyr	Gln	Arg	Glu	Asn	Pro	Thr	Glu	Lys	Gly	Leu	Asp	Phe	Lys	Leu	
			145					150					155			
tac	tgg	aca	gat	agc	caa	aac	aag	aaa	gaa	gtt	atc	agc	tca	gac	aat	531
Tyr	Trp	Thr	Asp	Ser	Gln	Asn	Lys	Lys	Glu	Val	Ile	Ser	Ser	Asp	Asn	
		160					165					170				
ctg	cag	tta	ccc	gag	ctc	aag	cag	aag	agt	tct	aat	aca	agc	gct	ggg	579
Leu	Gln	Leu	Pro	Glu	Leu	Lys	Gln	Lys	Ser	Ser	Asn	Thr	Ser	Ala	Gly	
	175					180					185					
cca	act	gtg	ccc	gac	aga	gac	aat	gat	gga	atc	cct	gat	agt	cta	gag	627
Pro	Thr	Val	Pro	Asp	Arg	Asp	Asn	Asp	Gly	Ile	Pro	Asp	Ser	Leu	Glu	
190				195						200					205	
gtt	gag	gga	tac	acg	gta	gat	gtc	aag	aac	aaa	agg	act	ttt	ctc	tcg	675
Val	Glu	Gly	Tyr	Thr	Val	Asp	Val	Lys	Asn	Lys	Arg	Thr	Phe	Leu	Ser	
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cct	tgg	atc	tca	aat	atc	cat	gag	aag	aag	ggg	ctt	acc	aag	tac	aag	723
Pro	Trp	Ile	Ser	Asn	Ile	His	Glu	Lys	Lys	Gly	Leu	Thr	Lys	Tyr	Lys	
			225					230					235			
tcc	tcc	ccc	gag	aag	tgg	tct	acc	gct	tcc	gat	cca	tat	agc	gat	ttc	771
Ser	Ser	Pro	Glu	Lys	Trp	Ser	Thr	Ala	Ser	Asp	Pro	Tyr	Ser	Asp	Phe	
		240					245					250				
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Glu	Lys	Val	Thr	Gly	Arg	Ile	Asp	Lys	Asn	Val	Ser	Pro	Glu	Ala	Arg	
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His	Pro	Leu	Val	Ala	Ala	Tyr	Pro	Ile	Val	His	Val	Asp	Met	Glu	Asn	
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atc	att	cta	agc	aaa	aac	gag	gac	cag	tcc	aca	caa	aac	act	gac	tcc	915
Ile	Ile	Leu	Ser	Lys	Asn	Glu	Asp	Gln	Ser	Thr	Gln	Asn	Thr	Asp	Ser	
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gag	acc	cgc	acc	ata	tct	aaa	aac	acc	agt	act	tca	agg	acc	cac	acc	963
Glu	Thr	Arg	Thr	Ile	Ser	Lys	Asn	Thr	Ser	Thr	Ser	Arg	Thr	His	Thr	
			305					310					315			
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Ser	Glu	Val	His	Gly	Asn	Ala	Glu	Val	His	Ala	Ser	Phe	Phe	Asp	Ile	
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Gly	Gly	Ser	Val	Ser	Ala	Gly	Phe	Ser	Asn	Ser	Asn	Ser	Ser	Thr	Val	
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gcc	att	gac	cac	tca	ctg	tca	tta	gca	ggt	gag	agg	act	tgg	gct	gaa	1107
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Thr Met Gly Leu Asn Thr Ala Asp Thr Ala Arg Leu Asn Ala Asn Ile							
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cgg tac gtc aac aca ggg act gct cct ata tat aac gtg ctg cct acg							1203
Arg Tyr Val Asn Thr Gly Thr Ala Pro Ile Tyr Asn Val Leu Pro Thr							
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aca agt ctt gtc ctg ggc aaa aat cag acc ctc gca acc att aag gca							1251
Thr Ser Leu Val Leu Gly Lys Asn Gln Thr Leu Ala Thr Ile Lys Ala							
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Lys Glu Asn Gln Leu Ser Gln Ile Leu Ala Pro Asn Asn Tyr Tyr Pro							
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tcc aaa aat tta gcc ccc ata gcc ctg aac gcc cag gac gac ttt tcc							1347
Ser Lys Asn Leu Ala Pro Ile Ala Leu Asn Ala Gln Asp Asp Phe Ser							
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tct acc ccc ata act atg aat tac aat cag ttc ctg gag ctg gaa aag							1395
Ser Thr Pro Ile Thr Met Asn Tyr Asn Gln Phe Leu Glu Leu Glu Lys							
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acg aag cag ctg aga cta gac acc gat cag gtg tat gga aac ata gcg							1443
Thr Lys Gln Leu Arg Leu Asp Thr Asp Gln Val Tyr Gly Asn Ile Ala							
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aca tat aac ttt gag aac ggc cgc gtg cgc gtc gac act ggg tca aac							1491
Thr Tyr Asn Phe Glu Asn Gly Arg Val Arg Val Asp Thr Gly Ser Asn							
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Trp Ser Glu Val Leu Pro Gln Ile Gln Glu Thr Thr Ala Arg Ile Ile							
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Phe Asn Gly Lys Asp Leu Asn Leu Val Glu Arg Arg Ile Ala Ala Val							
		510		515		520	
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Glu Ala Leu Lys Ile Ala Phe Gly Phe Asn Glu Pro Asn Gly Asn Leu							
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Gln Tyr Gln Gly Lys Asp Ile Thr Glu Phe Asp Phe Asn Phe Asp Gln							
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Gln Thr Ser Gln Asn Ile Lys Asn Gln Leu Ala Glu Leu Asn Ala Thr							
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aat atc tac acg gtt ctc gat aaa atc aaa ctt aac gcc aag atg aac							1827
Asn Ile Tyr Thr Val Leu Asp Lys Ile Lys Leu Asn Ala Lys Met Asn							
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						605	

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aag atc ctg tcc ggg tat atc gtg gag atc gag gat acc gag ggc ctg Lys Ile Leu Ser Gly Tyr Ile Val Glu Ile Glu Asp Thr Glu Gly Leu 655 660 665	2019
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cga cag gac ggt aag aca ttt att gac ttt aaa aag tat aac gac aag Arg Gln Asp Gly Lys Thr Phe Ile Asp Phe Lys Lys Tyr Asn Asp Lys 690 695 700	2115
cta ccc ctg tac att tcc aac cca aat tac aaa gtt aat gtg tat gct Leu Pro Leu Tyr Ile Ser Asn Pro Asn Tyr Lys Val Asn Val Tyr Ala 705 710 715	2163
gta acc aag gag aac aca atc atc aat cca agc gag aac ggc gat acc Val Thr Lys Glu Asn Thr Ile Ile Asn Pro Ser Glu Asn Gly Asp Thr 720 725 730	2211
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<213> Artificial Sequence

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25

30

Asn Glu Ser Glu Ser Ser Ser Gln Gly Leu Leu Gly Tyr Tyr Phe Ser
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Asp Leu Asn Phe Gln Ala Pro Met Val Val Thr Ser Ser Thr Thr Gly
50 55 60

Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu Asn Ile Pro Ser Glu Asn
65 70 75 80

Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly Phe Ile Lys Val Lys Lys
85 90 95

Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala Asp Asn His Val Thr Met
100 105 110

Trp Val Asp Asp Gln Glu Val Ile Asn Lys Ala Ser Asn Ser Asn Lys
115 120 125

Ile Arg Leu Glu Lys Gly Arg Leu Tyr Gln Ile Lys Ile Gln Tyr Gln
130 135 140

Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp Phe Lys Leu Tyr Trp Thr
145 150 155 160

Asp Ser Gln Asn Lys Lys Glu Val Ile Ser Ser Asp Asn Leu Gln Leu
165 170 175

Pro Glu Leu Lys Gln Lys Ser Ser Asn Thr Ser Ala Gly Pro Thr Val
180 185 190

Pro Asp Arg Asp Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly
195 200 205

Tyr Thr Val Asp Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile
210 215 220

Ser Asn Ile His Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro
225 230 235 240

Glu Lys Trp Ser Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val
245 250 255

Thr Gly Arg Ile Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu
260 265 270

Val	Ala	Ala	Tyr	Pro	Ile	Val	His	Val	Asp	Met	Glu	Asn	Ile	Ile	Leu
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Ser	Lys	Asn	Glu	Asp	Gln	Ser	Thr	Gln	Asn	Thr	Asp	Ser	Glu	Thr	Arg
	290					295					300				
Thr	Ile	Ser	Lys	Asn	Thr	Ser	Thr	Ser	Arg	Thr	His	Thr	Ser	Glu	Val
305					310					315					320
His	Gly	Asn	Ala	Glu	Val	His	Ala	Ser	Phe	Phe	Asp	Ile	Gly	Gly	Ser
				325					330					335	
Val	Ser	Ala	Gly	Phe	Ser	Asn	Ser	Asn	Ser	Ser	Thr	Val	Ala	Ile	Asp
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His	Ser	Leu	Ser	Leu	Ala	Gly	Glu	Arg	Thr	Trp	Ala	Glu	Thr	Met	Gly
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Leu	Asn	Thr	Ala	Asp	Thr	Ala	Arg	Leu	Asn	Ala	Asn	Ile	Arg	Tyr	Val
	370					375					380				
Asn	Thr	Gly	Thr	Ala	Pro	Ile	Tyr	Asn	Val	Leu	Pro	Thr	Thr	Ser	Leu
385					390					395					400
Val	Leu	Gly	Lys	Asn	Gln	Thr	Leu	Ala	Thr	Ile	Lys	Ala	Lys	Glu	Asn
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Gln	Leu	Ser	Gln	Ile	Leu	Ala	Pro	Asn	Asn	Tyr	Tyr	Pro	Ser	Lys	Asn
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Leu	Ala	Pro	Ile	Ala	Leu	Asn	Ala	Gln	Asp	Asp	Phe	Ser	Ser	Thr	Pro
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Ile	Thr	Met	Asn	Tyr	Asn	Gln	Phe	Leu	Glu	Leu	Glu	Lys	Thr	Lys	Gln
	450					455					460				
Leu	Arg	Leu	Asp	Thr	Asp	Gln	Val	Tyr	Gly	Asn	Ile	Ala	Thr	Tyr	Asn
465					470					475					480
Phe	Glu	Asn	Gly	Arg	Val	Arg	Val	Asp	Thr	Gly	Ser	Asn	Trp	Ser	Glu
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Val	Leu	Pro	Gln	Ile	Gln	Glu	Thr	Thr	Ala	Arg	Ile	Ile	Phe	Asn	Gly
			500					505					510		
Lys	Asp	Leu	Asn	Leu	Val	Glu	Arg	Arg	Ile	Ala	Ala	Val	Asn	Pro	Ser
		515					520					525			

Asp Pro Leu Glu Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu
530 535 540

Lys Ile Ala Phe Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln
545 550 555 560

Gly Lys Asp Ile Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser
565 570 575

Gln Asn Ile Lys Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr
580 585 590

Thr Val Leu Asp Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile
595 600 605

Arg Asp Lys Arg Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala
610 615 620

Asp Glu Ser Val Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser
625 630 635 640

Thr Glu Gly Leu Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu
645 650 655

Ser Gly Tyr Ile Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val
660 665 670

Ile Asn Asp Arg Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp
675 680 685

Gly Lys Thr Phe Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu
690 695 700

Tyr Ile Ser Asn Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys
705 710 715 720

Glu Asn Thr Ile Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn
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<211> 2418

<212> DNA

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<220>

<223> Synthetic coding region for Human TPA/synthetic antigen fusion protein

<220>

<221> CDS

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Leu Cys Gly Ala Val Phe Val Ser Pro Ser Ala Gly Gly His Gly Asp	
15 20 25	
gtt ggc atg cat gtg aaa gaa aag gag aaa aac aag gac gaa aac aag	147
Val Gly Met His Val Lys Glu Lys Glu Lys Asn Lys Asp Glu Asn Lys	
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Arg Lys Asp Glu Glu Arg Asn Lys Thr Gln Glu Glu His Leu Lys Glu	
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atc atg aag cac ata gta aag att gag gta aaa ggc gaa gag gct gta	243
Ile Met Lys His Ile Val Lys Ile Glu Val Lys Gly Glu Glu Ala Val	
65 70 75	
aag aag gag gca gca gaa aaa ctg ttg gag aag gtg cct tct gac gtc	291
Lys Lys Glu Ala Ala Glu Lys Leu Leu Glu Lys Val Pro Ser Asp Val	
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Leu Glu Met Tyr Lys Ala Ile Gly Gly Lys Ile Tyr Ile Val Asp Gly	
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gac atc act aaa cac ata tct ctc gaa gct ctc tcc gag gac aag aaa	387
Asp Ile Thr Lys His Ile Ser Leu Glu Ala Leu Ser Glu Asp Lys Lys	
110 115 120 125	
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Lys Ile Lys Asp Ile Tyr Gly Lys Asp Ala Leu Leu His Glu His Tyr	
130 135 140	
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Val Tyr Ala Lys Glu Gly Tyr Glu Pro Val Leu Val Ile Gln Ser Ser	
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Glu Asp Tyr Val Glu Asn Thr Glu Lys Ala Leu Asn Val Tyr Tyr Glu	

160	165	170	
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			20					25					30		

His Val Lys Glu Lys Glu Lys Asn Lys Asp Glu Asn Lys Arg Lys Asp
35 40 45

Glu Glu Arg Asn Lys Thr Gln Glu Glu His Leu Lys Glu Ile Met Lys
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His Ile Val Lys Ile Glu Val Lys Gly Glu Glu Ala Val Lys Lys Glu
65 70 75 80

Ala Ala Glu Lys Leu Leu Glu Lys Val Pro Ser Asp Val Leu Glu Met
85 90 95

Tyr Lys Ala Ile Gly Gly Lys Ile Tyr Ile Val Asp Gly Asp Ile Thr
100 105 110

Lys His Ile Ser Leu Glu Ala Leu Ser Glu Asp Lys Lys Lys Ile Lys
115 120 125

Asp Ile Tyr Gly Lys Asp Ala Leu Leu His Glu His Tyr Val Tyr Ala
130 135 140

Lys Glu Gly Tyr Glu Pro Val Leu Val Ile Gln Ser Ser Glu Asp Tyr
145 150 155 160

Val Glu Asn Thr Glu Lys Ala Leu Asn Val Tyr Tyr Glu Ile Gly Lys
165 170 175

Ile Leu Ser Arg Asp Ile Leu Ser Lys Ile Asn Gln Pro Tyr Gln Lys
180 185 190

Phe Leu Asp Val Leu Asn Thr Ile Lys Asn Ala Ser Asp Ser Asp Gly
195 200 205

Gln Asp Leu Leu Phe Thr Asn Gln Leu Lys Glu His Pro Thr Asp Phe
210 215 220

Ser Val Glu Phe Leu Glu Gln Asn Ser Asn Glu Val Gln Glu Val Phe
225 230 235 240

Ala Lys Ala Phe Ala Tyr Tyr Ile Glu Pro Gln His Arg Asp Val Leu
245 250 255

Gln Leu Tyr Ala Pro Glu Ala Phe Asn Tyr Met Asp Lys Phe Asn Glu
260 265 270

Gln Glu Ile Asn Leu Ser Leu Glu Glu Leu Lys Asp Gln Arg Met Leu
275 280 285

Ser Arg Tyr Glu Lys Trp Glu Lys Ile Lys Gln His Tyr Gln His Trp
290 295 300

Ser Asp Ser Leu Ser Glu Glu Gly Arg Gly Leu Leu Lys Lys Leu Gln
305 310 315 320

Ile Pro Ile Glu Pro Lys Lys Asp Asp Ile Ile His Ser Leu Ser Gln
325 330 335

Glu Glu Lys Glu Leu Leu Lys Arg Ile Gln Ile Asp Ser Ser Asp Phe
340 345 350

Leu Ser Thr Glu Glu Lys Glu Phe Leu Lys Lys Leu Gln Ile Asp Ile
355 360 365

Arg Asp Ser Leu Ser Glu Glu Glu Lys Glu Leu Leu Asn Arg Ile Gln
370 375 380

Val Asp Ser Ser Asn Pro Leu Ser Glu Lys Glu Lys Glu Phe Leu Lys
385 390 395 400

Lys Leu Lys Leu Asp Ile Gln Pro Tyr Asp Ile Asn Gln Arg Leu Gln
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Asp Thr Gly Gly Leu Ile Asp Ser Pro Ser Ile Asn Leu Asp Val Arg
420 425 430

Lys Gln Tyr Lys Arg Asp Ile Gln Asn Ile Asp Ala Leu Leu His Gln
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Ser Ile Gly Ser Thr Leu Tyr Asn Lys Ile Tyr Leu Tyr Glu Asn Met
450 455 460

Asn Ile Asn Asn Leu Thr Ala Thr Leu Gly Ala Asp Leu Val Asp Ser
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Thr Asp Asn Thr Lys Ile Asn Arg Gly Ile Phe Asn Glu Phe Lys Lys
485 490 495

Asn Phe Lys Tyr Ser Ile Ser Ser Asn Tyr Met Ile Val Asp Ile Asn
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Glu Arg Pro Ala Leu Asp Asn Glu Arg Leu Lys Trp Arg Ile Gln Leu
515 520 525

Ser Pro Asp Thr Arg Ala Gly Tyr Leu Glu Asn Gly Lys Leu Ile Leu

530	535	540
Gln Arg Asn Ile Gly Leu Glu Ile Lys Asp Val Gln Ile Ile Lys Gln		
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Ser Glu Lys Glu Tyr Ile Arg Ile Asp Ala Lys Val Val Pro Lys Ser		
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Lys Ile Asp Thr Lys Ile Gln Glu Ala Gln Leu Asn Ile Asn Gln Glu		
	580	585 590
Trp Asn Lys Ala Leu Gly Leu Pro Lys Tyr Thr Lys Leu Ile Thr Phe		
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Asn Val His Asn Arg Tyr Ala Ser Asn Ile Val Glu Ser Ala Tyr Leu		
	610	615 620
Ile Leu Asn Glu Trp Lys Asn Asn Ile Gln Ser Asp Leu Ile Lys Lys		
625	630	635 640
Val Thr Asn Tyr Leu Val Asp Gly Asn Gly Arg Phe Val Phe Thr Asp		
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Ile Thr Leu Pro Asn Ile Ala Glu Gln Tyr Thr His Gln Asp Glu Ile		
	660	665 670
Tyr Glu Gln Val His Ser Lys Gly Leu Tyr Val Pro Glu Ser Arg Ser		
	675	680 685
Ile Leu Leu His Gly Pro Ser Lys Gly Val Glu Leu Arg Asn Asp Ser		
690	695	700
Glu Gly Phe Ile Ala Asp Phe Gly Ala Ala Val Asp Asp Tyr Ala Gly		
705	710	715 720
Tyr Leu Leu Asp Lys Asn Gln Ser Asp Leu Val Thr Asn Ser Lys Lys		
	725	730 735
Phe Ile Asp Ile Phe Lys Glu Glu Gly Ser Asn Leu Thr Ser Tyr Gly		
	740	745 750
Arg Thr Asn Glu Ala Glu Phe Phe Ala Glu Ala Phe Arg Leu Met His		
	755	760 765
Ser Thr Asp His Ala Glu Arg Leu Lys Val Gln Lys Asn Ala Pro Lys		
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Thr Phe Gln Phe Ile Asn Asp Gln Ile Lys Phe Ile Ile Asn Ser
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<212> DNA

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<220>

<221> CDS

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ttccatagaa attaatcctt ttgttataca tctttattcc cttaacattg tcaaatttca 180
gttattcatt ctggatagtc aataaataga ttacggttat gttagtattt ttttaaaata 240
atagtattaa atagtggaat gcaaatgata aatgggcttt aaacaaaact aatgaaataa 300
tctacaaatg gaatttctcc agtttttagat taaaccatac caaaaaaatc acactgtcaa 360
gaaaaatgat agaatcccta cactaattaa cataaccaaa ttggtagtta taggtagaaa 420
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tagtaaatta tttagcaagt aaattttggt gtataaacia agttttatctt aatataaaaa 540
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taatttatga ggaaataagt aaaattttct acatacttta ttttattggt gaaatgttca 660
cttataaaaa aggagagatt aaat atg aat ata aaa aaa gaa ttt ata aaa 711
Met Asn Ile Lys Lys Glu Phe Ile Lys
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gta att agt atg tca tgt tta gta aca gca att act ttg agt ggt ccc 759
Val Ile Ser Met Ser Cys Leu Val Thr Ala Ile Thr Leu Ser Gly Pro
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gtc ttt atc ccc ctt gta cag ggg gcg ggc ggt cat ggt gat gta ggt 807
Val Phe Ile Pro Leu Val Gln Gly Ala Gly Gly His Gly Asp Val Gly
30 35 40
atg cac gta aaa gag aaa gag aaa aat aaa gat gag aat aag aga aaa 855
Met His Val Lys Glu Lys Glu Lys Asn Lys Asp Glu Asn Lys Arg Lys
45 50 55

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gag gca gca gaa aag cta ctt gag aaa gta cca tct gat gtt tta gag Glu Ala Ala Glu Lys Leu Leu Glu Lys Val Pro Ser Asp Val Leu Glu 90 95 100 105	999
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aca aaa cat ata tct tta gaa gca tta tct gaa gat aag aaa aaa ata Thr Lys His Ile Ser Leu Glu Ala Leu Ser Glu Asp Lys Lys Lys Ile 125 130 135	1095
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gaa caa gaa ata aat cta tcc ttg gaa gaa ctt aaa gat caa cgg atg Glu Gln Glu Ile Asn Leu Ser Leu Glu Glu Leu Lys Asp Gln Arg Met 285 290 295	1575
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Leu	Gln	Arg	Asn	Ile	Gly	Leu	Glu	Ile	Lys	Asp	Val	Gln	Ile	Ile	Lys	
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gaa	tgg	aat	aaa	gca	tta	ggg	tta	cca	aaa	tat	aca	aag	ctt	att	aca	2535
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Lys	Val	Thr	Asn	Tyr	Leu	Val	Asp	Gly	Asn	Gly	Arg	Phe	Val	Phe	Thr	
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Asp	Ile	Thr	Leu	Pro	Asn	Ile	Ala	Glu	Gln	Tyr	Thr	His	Gln	Asp	Glu	
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ata	tat	gag	caa	gtt	cat	tca	aaa	ggg	tta	tat	gtt	cca	gaa	tcc	cgt	2775
Ile	Tyr	Glu	Gln	Val	His	Ser	Lys	Gly	Leu	Tyr	Val	Pro	Glu	Ser	Arg	
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tct	ata	tta	ctc	cat	gga	cct	tca	aaa	ggg	gta	gaa	tta	agg	aat	gat	2823
Ser	Ile	Leu	Leu	His	Gly	Pro	Ser	Lys	Gly	Val	Glu	Leu	Arg	Asn	Asp	
		700					705					710				
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Ser	Glu	Gly	Phe	Ile	His	Glu	Phe	Gly	His	Ala	Val	Asp	Asp	Tyr	Ala	
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gga	tat	cta	tta	gat	aag	aac	caa	tct	gat	tta	gtt	aca	aat	tct	aaa	2919
Gly	Tyr	Leu	Leu	Asp	Lys	Asn	Gln	Ser	Asp	Leu	Val	Thr	Asn	Ser	Lys	
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Lys	Phe	Ile	Asp	Ile	Phe	Lys	Glu	Glu	Gly	Ser	Asn	Leu	Thr	Ser	Tyr	
				750					755					760		
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Gly	Arg	Thr	Asn	Glu	Ala	Glu	Phe	Phe	Ala	Glu	Ala	Phe	Arg	Leu	Met	
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cat	tct	acg	gac	cat	gct	gaa	cgt	tta	aaa	gtt	caa	aaa	aat	gct	ccg	3063
His	Ser	Thr	Asp	His	Ala	Glu	Arg	Leu	Lys	Val	Gln	Lys	Asn	Ala	Pro	
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Lys	Thr	Phe	Gln	Phe	Ile	Asn	Asp	Gln	Ile	Lys	Phe	Ile	Ile	Asn	Ser	

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Lys	Asn	Lys	Asp	Glu	Asn	Lys	Arg	Lys	Asp	Glu	Glu	Arg	Asn	Lys	Thr
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Gln	Glu	Glu	His	Leu	Lys	Glu	Ile	Met	Lys	His	Ile	Val	Lys	Ile	Glu
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Val	Lys	Gly	Glu	Glu	Ala	Val	Lys	Lys	Glu	Ala	Ala	Glu	Lys	Leu	Leu
				85					90					95	

Glu	Lys	Val	Pro	Ser	Asp	Val	Leu	Glu	Met	Tyr	Lys	Ala	Ile	Gly	Gly
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Lys	Ile	Tyr	Ile	Val	Asp	Gly	Asp	Ile	Thr	Lys	His	Ile	Ser	Leu	Glu
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Val Leu Val Ile Gln Ser Ser Glu Asp Tyr Val Glu Asn Thr Glu Lys				
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Ala Leu Asn Val Tyr Tyr Glu Ile Gly Lys Ile Leu Ser Arg Asp Ile				
		180		185
Leu Ser Lys Ile Asn Gln Pro Tyr Gln Lys Phe Leu Asp Val Leu Asn				
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Thr Ile Lys Asn Ala Ser Asp Ser Asp Gly Gln Asp Leu Leu Phe Thr				
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Asn Gln Leu Lys Glu His Pro Thr Asp Phe Ser Val Glu Phe Leu Glu				
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Gln Asn Ser Asn Glu Val Gln Glu Val Phe Ala Lys Ala Phe Ala Tyr				
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Tyr Ile Glu Pro Gln His Arg Asp Val Leu Gln Leu Tyr Ala Pro Glu				
		260		265
Ala Phe Asn Tyr Met Asp Lys Phe Asn Glu Gln Glu Ile Asn Leu Ser				
		275		280
Leu Glu Glu Leu Lys Asp Gln Arg Met Leu Ser Arg Tyr Glu Lys Trp				
		290		295
Glu Lys Ile Lys Gln His Tyr Gln His Trp Ser Asp Ser Leu Ser Glu				
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Glu Gly Arg Gly Leu Leu Lys Lys Leu Gln Ile Pro Ile Glu Pro Lys				
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Lys Asp Asp Ile Ile His Ser Leu Ser Gln Glu Glu Lys Glu Leu Leu				
		340		345
Lys Arg Ile Gln Ile Asp Ser Ser Asp Phe Leu Ser Thr Glu Glu Lys				
		355		360

Glu Phe Leu Lys Lys Leu Gln Ile Asp Ile Arg Asp Ser Leu Ser Glu
370 375 380

Glu Glu Lys Glu Leu Leu Asn Arg Ile Gln Val Asp Ser Ser Asn Pro
385 390 395 400

Leu Ser Glu Lys Glu Lys Glu Phe Leu Lys Lys Leu Lys Leu Asp Ile
405 410 415

Gln Pro Tyr Asp Ile Asn Gln Arg Leu Gln Asp Thr Gly Gly Leu Ile
420 425 430

Asp Ser Pro Ser Ile Asn Leu Asp Val Arg Lys Gln Tyr Lys Arg Asp
435 440 445

Ile Gln Asn Ile Asp Ala Leu Leu His Gln Ser Ile Gly Ser Thr Leu
450 455 460

Tyr Asn Lys Ile Tyr Leu Tyr Glu Asn Met Asn Ile Asn Asn Leu Thr
465 470 475 480

Ala Thr Leu Gly Ala Asp Leu Val Asp Ser Thr Asp Asn Thr Lys Ile
485 490 495

Asn Arg Gly Ile Phe Asn Glu Phe Lys Lys Asn Phe Lys Tyr Ser Ile
500 505 510

Ser Ser Asn Tyr Met Ile Val Asp Ile Asn Glu Arg Pro Ala Leu Asp
515 520 525

Asn Glu Arg Leu Lys Trp Arg Ile Gln Leu Ser Pro Asp Thr Arg Ala
530 535 540

Gly Tyr Leu Glu Asn Gly Lys Leu Ile Leu Gln Arg Asn Ile Gly Leu
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Glu Ile Lys Asp Val Gln Ile Ile Lys Gln Ser Glu Lys Glu Tyr Ile
565 570 575

Arg Ile Asp Ala Lys Val Val Pro Lys Ser Lys Ile Asp Thr Lys Ile
580 585 590

Gln Glu Ala Gln Leu Asn Ile Asn Gln Glu Trp Asn Lys Ala Leu Gly
595 600 605

Leu Pro Lys Tyr Thr Lys Leu Ile Thr Phe Asn Val His Asn Arg Tyr
610 615 620

Ala Ser Asn Ile Val Glu Ser Ala Tyr Leu Ile Leu Asn Glu Trp Lys
625 630 635 640

Asn Asn Ile Gln Ser Asp Leu Ile Lys Lys Val Thr Asn Tyr Leu Val
645 650 655

Asp Gly Asn Gly Arg Phe Val Phe Thr Asp Ile Thr Leu Pro Asn Ile
660 665 670

Ala Glu Gln Tyr Thr His Gln Asp Glu Ile Tyr Glu Gln Val His Ser
675 680 685

Lys Gly Leu Tyr Val Pro Glu Ser Arg Ser Ile Leu Leu His Gly Pro
690 695 700

Ser Lys Gly Val Glu Leu Arg Asn Asp Ser Glu Gly Phe Ile His Glu
705 710 715 720

Phe Gly His Ala Val Asp Asp Tyr Ala Gly Tyr Leu Leu Asp Lys Asn
725 730 735

Gln Ser Asp Leu Val Thr Asn Ser Lys Lys Phe Ile Asp Ile Phe Lys
740 745 750

Glu Glu Gly Ser Asn Leu Thr Ser Tyr Gly Arg Thr Asn Glu Ala Glu
755 760 765

Phe Phe Ala Glu Ala Phe Arg Leu Met His Ser Thr Asp His Ala Glu
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antigen fusion protein

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ggt ggc atg cat gtg aaa gaa aag gag aaa aac aag gac gaa aac aag	147
Val Gly Met His Val Lys Glu Lys Glu Lys Asn Lys Asp Glu Asn Lys	
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Arg Lys Asp Glu Glu Arg Asn Lys Thr Gln Glu Glu His Leu Lys Glu	
50 55 60	
atc atg aag cac ata gta aag att gag gta aaa ggc gaa gag gct gta	243
Ile Met Lys His Ile Val Lys Ile Glu Val Lys Gly Glu Glu Ala Val	
65 70 75	
aag aag gag gca gca gaa aaa ctg ttg gag aag gtg cct tct gac gtc	291
Lys Lys Glu Ala Ala Glu Lys Leu Leu Glu Lys Val Pro Ser Asp Val	
80 85 90	
tta gag atg tat aag gcc atc ggc ggt aag atc tat atc gtg gac gga	339
Leu Glu Met Tyr Lys Ala Ile Gly Gly Lys Ile Tyr Ile Val Asp Gly	
95 100 105	
gac atc act aaa cac ata tct ctc gaa gct ctc tcc gag gac aag aaa	387
Asp Ile Thr Lys His Ile Ser Leu Glu Ala Leu Ser Glu Asp Lys Lys	
110 115 120 125	
aag att aaa gac atc tac ggg aag gat gcc tta ttg cac gag cac tac	435
Lys Ile Lys Asp Ile Tyr Gly Lys Asp Ala Leu Leu His Glu His Tyr	
130 135 140	
ggt tac gca aag gag ggc tat gag ccc gtg ctc gtt att cag agt agt	483
Val Tyr Ala Lys Glu Gly Tyr Glu Pro Val Leu Val Ile Gln Ser Ser	
145 150 155	
gag gac tac gtc gag aat acc gag aaa gct ctg aat gtg tat tac gag	531
Glu Asp Tyr Val Glu Asn Thr Glu Lys Ala Leu Asn Val Tyr Tyr Glu	
160 165 170	
atc gga aag att ctg tcc cgg gac atc ctg tcc aaa atc aac cag cca	579
Ile Gly Lys Ile Leu Ser Arg Asp Ile Leu Ser Lys Ile Asn Gln Pro	
175 180 185	
tac cag aaa ttc ctt gat gtt ctt aac aca atc aaa aac gcg tca gat	627

Tyr	Gln	Lys	Phe	Leu	Asp	Val	Leu	Asn	Thr	Ile	Lys	Asn	Ala	Ser	Asp	
190					195					200					205	
agc	gac	ggg	cag	gat	ctt	ctg	ttt	aca	aat	caa	ctc	aag	gaa	cac	ccc	675
Ser	Asp	Gly	Gln	Asp	Leu	Leu	Phe	Thr	Asn	Gln	Leu	Lys	Glu	His	Pro	
				210					215					220		
act	gat	ttc	agc	gtg	gag	ttc	ctc	gag	cag	aat	tct	aac	gaa	gtc	cag	723
Thr	Asp	Phe	Ser	Val	Glu	Phe	Leu	Glu	Gln	Asn	Ser	Asn	Glu	Val	Gln	
			225					230					235			
gag	gtg	ttc	gcc	aag	gca	ttt	gcg	tac	tat	atc	gaa	ccc	cag	cat	cgc	771
Glu	Val	Phe	Ala	Lys	Ala	Phe	Ala	Tyr	Tyr	Ile	Glu	Pro	Gln	His	Arg	
		240					245					250				
gat	gtg	ctc	cag	ctg	tac	gcc	ccg	gag	gca	ttt	aac	tac	atg	gac	aaa	819
Asp	Val	Leu	Gln	Leu	Tyr	Ala	Pro	Glu	Ala	Phe	Asn	Tyr	Met	Asp	Lys	
	255					260					265					
ttc	aat	gaa	cag	gag	att	aat	ctg	tct	ctg	gag	gaa	ctg	aaa	gac	cag	867
Phe	Asn	Glu	Gln	Glu	Ile	Asn	Leu	Ser	Leu	Glu	Glu	Leu	Lys	Asp	Gln	
270					275					280					285	
agg	atg	ctc	tcc	cgg	tat	gaa	aag	tgg	gaa	aag	atc	aaa	cag	cat	tac	915
Arg	Met	Leu	Ser	Arg	Tyr	Glu	Lys	Trp	Glu	Lys	Ile	Lys	Gln	His	Tyr	
				290					295					300		
cag	cat	tgg	tcc	gac	tcc	ctg	tca	gaa	gag	ggg	cgc	ggc	ctg	ttg	aaa	963
Gln	His	Trp	Ser	Asp	Ser	Leu	Ser	Glu	Glu	Gly	Arg	Gly	Leu	Leu	Lys	
			305					310					315			
aag	ttg	cag	att	ccc	atc	gag	cct	aag	aaa	gat	gat	ata	ata	cac	tct	1011
Lys	Leu	Gln	Ile	Pro	Ile	Glu	Pro	Lys	Lys	Asp	Asp	Ile	Ile	His	Ser	
		320					325					330				
cta	agc	cag	gag	gag	aag	gaa	ctc	ctg	aag	cgg	ata	caa	atc	gac	tca	1059
Leu	Ser	Gln	Glu	Glu	Lys	Glu	Leu	Leu	Lys	Arg	Ile	Gln	Ile	Asp	Ser	
	335					340					345					
tcc	gat	ttc	ctt	agc	aca	gaa	gag	aag	gag	ttt	cta	aaa	aaa	ctt	cag	1107
Ser	Asp	Phe	Leu	Ser	Thr	Glu	Glu	Lys	Glu	Phe	Leu	Lys	Lys	Leu	Gln	
350					355					360					365	
ata	gat	att	aga	gat	tca	ctg	agc	gag	gaa	gag	aag	gag	ctg	ctc	aac	1155
Ile	Asp	Ile	Arg	Asp	Ser	Leu	Ser	Glu	Glu	Glu	Lys	Glu	Leu	Leu	Asn	
				370					375					380		
cga	att	caa	gtc	gat	agt	tcg	aac	ccc	ttg	tca	gaa	aaa	gag	aag	gaa	1203
Arg	Ile	Gln	Val	Asp	Ser	Ser	Asn	Pro	Leu	Ser	Glu	Lys	Glu	Lys	Glu	
			385					390					395			
ttc	ctg	aaa	aag	ttg	aag	ctc	gac	atc	cag	ccg	tac	gat	att	aat	cag	1251
Phe	Leu	Lys	Lys	Leu	Lys	Leu	Asp	Ile	Gln	Pro	Tyr	Asp	Ile	Asn	Gln	
		400					405					410				
cgg	cta	caa	gac	acc	ggc	ggg	ctg	att	gat	agc	ccc	agc	atc	aac	ctt	1299
Arg	Leu	Gln	Asp	Thr	Gly	Gly	Leu	Ile	Asp	Ser	Pro	Ser	Ile	Asn	Leu	
	415					420					425					
gac	gta	cgg	aag	caa	tat	aag	cgc	gac	att	caa	aat	atc	gac	gcc	cta	1347
Asp	Val	Arg	Lys	Gln	Tyr	Lys	Arg	Asp	Ile	Gln	Asn	Ile	Asp	Ala	Leu	
430					435					440					445	

tta cat caa tcc ata ggc tcc acg cta tac aat aaa atc tat cta tac	1395
Leu His Gln Ser Ile Gly Ser Thr Leu Tyr Asn Lys Ile Tyr Leu Tyr	
450 455 460	
gaa aac atg aat att aac aat ctc acc gct aca ctg gga gcg gac ctg	1443
Glu Asn Met Asn Ile Asn Asn Leu Thr Ala Thr Leu Gly Ala Asp Leu	
465 470 475	
gtc gat agt aca gac aac aca aag ata aac aga ggt att ttc aac gaa	1491
Val Asp Ser Thr Asp Asn Thr Lys Ile Asn Arg Gly Ile Phe Asn Glu	
480 485 490	
ttc aaa aag aac ttt aag tat tcg atc agc agt aac tat atg att gtt	1539
Phe Lys Lys Asn Phe Lys Tyr Ser Ile Ser Ser Asn Tyr Met Ile Val	
495 500 505	
gac atc aat gaa cgg ccc gca tta gac aat gag agg ttg aag tgg aga	1587
Asp Ile Asn Glu Arg Pro Ala Leu Asp Asn Glu Arg Leu Lys Trp Arg	
510 515 520 525	
att caa ctg agt cct gat act agg gcc ggc tat ctg gag aac ggg aaa	1635
Ile Gln Leu Ser Pro Asp Thr Arg Ala Gly Tyr Leu Glu Asn Gly Lys	
530 535 540	
ctg atc tta cag cga aac atc ggg ctg gag atc aag gat gtg cag att	1683
Leu Ile Leu Gln Arg Asn Ile Gly Leu Glu Ile Lys Asp Val Gln Ile	
545 550 555	
atc aag cag agc gaa aaa gaa tac att cgc atc gac gcc aag gtg gtg	1731
Ile Lys Gln Ser Glu Lys Glu Tyr Ile Arg Ile Asp Ala Lys Val Val	
560 565 570	
tagggatcc	1740

<210> 14

<211> 573

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TPA/B. anthracis antigen fusion protein

<400> 14

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
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Ala Val Phe Val Ser Pro Ser Ala Gly Gly His Gly Asp Val Gly Met
20 25 30

His Val Lys Glu Lys Glu Lys Asn Lys Asp Glu Asn Lys Arg Lys Asp
35 40 45

Glu	Glu	Arg	Asn	Lys	Thr	Gln	Glu	Glu	His	Leu	Lys	Glu	Ile	Met	Lys	
50						55					60					
His	Ile	Val	Lys	Ile	Glu	Val	Lys	Gly	Glu	Glu	Ala	Val	Lys	Lys	Glu	
65					70					75					80	
Ala	Ala	Glu	Lys	Leu	Leu	Glu	Lys	Val	Pro	Ser	Asp	Val	Leu	Glu	Met	
				85					90					95		
Tyr	Lys	Ala	Ile	Gly	Gly	Lys	Ile	Tyr	Ile	Val	Asp	Gly	Asp	Ile	Thr	
			100					105					110			
Lys	His	Ile	Ser	Leu	Glu	Ala	Leu	Ser	Glu	Asp	Lys	Lys	Lys	Ile	Lys	
		115					120					125				
Asp	Ile	Tyr	Gly	Lys	Asp	Ala	Leu	Leu	His	Glu	His	Tyr	Val	Tyr	Ala	
	130					135					140					
Lys	Glu	Gly	Tyr	Glu	Pro	Val	Leu	Val	Ile	Gln	Ser	Ser	Glu	Asp	Tyr	
145					150					155					160	
Val	Glu	Asn	Thr	Glu	Lys	Ala	Leu	Asn	Val	Tyr	Tyr	Glu	Ile	Gly	Lys	
				165					170					175		
Ile	Leu	Ser	Arg	Asp	Ile	Leu	Ser	Lys	Ile	Asn	Gln	Pro	Tyr	Gln	Lys	
			180					185					190			
Phe	Leu	Asp	Val	Leu	Asn	Thr	Ile	Lys	Asn	Ala	Ser	Asp	Ser	Asp	Gly	
		195					200					205				
Gln	Asp	Leu	Leu	Phe	Thr	Asn	Gln	Leu	Lys	Glu	His	Pro	Thr	Asp	Phe	
	210					215					220					
Ser	Val	Glu	Phe	Leu	Glu	Gln	Asn	Ser	Asn	Glu	Val	Gln	Glu	Val	Phe	
225					230					235					240	
Ala	Lys	Ala	Phe	Ala	Tyr	Tyr	Ile	Glu	Pro	Gln	His	Arg	Asp	Val	Leu	
				245					250					255		
Gln	Leu	Tyr	Ala	Pro	Glu	Ala	Phe	Asn	Tyr	Met	Asp	Lys	Phe	Asn	Glu	
			260					265					270			
Gln	Glu	Ile	Asn	Leu	Ser	Leu	Glu	Glu	Leu	Lys	Asp	Gln	Arg	Met	Leu	
	275						280					285				
Ser	Arg	Tyr	Glu	Lys	Trp	Glu	Lys	Ile	Lys	Gln	His	Tyr	Gln	His	Trp	
	290					295					300					

Ser Asp Ser Leu Ser Glu Glu Gly Arg Gly Leu Leu Lys Lys Leu Gln
305 310 315 320

Ile Pro Ile Glu Pro Lys Lys Asp Asp Ile Ile His Ser Leu Ser Gln
325 330 335

Glu Glu Lys Glu Leu Leu Lys Arg Ile Gln Ile Asp Ser Ser Asp Phe
340 345 350

Leu Ser Thr Glu Glu Lys Glu Phe Leu Lys Lys Leu Gln Ile Asp Ile
355 360 365

Arg Asp Ser Leu Ser Glu Glu Glu Lys Glu Leu Leu Asn Arg Ile Gln
370 375 380

Val Asp Ser Ser Asn Pro Leu Ser Glu Lys Glu Lys Glu Phe Leu Lys
385 390 395 400

Lys Leu Lys Leu Asp Ile Gln Pro Tyr Asp Ile Asn Gln Arg Leu Gln
405 410 415

Asp Thr Gly Gly Leu Ile Asp Ser Pro Ser Ile Asn Leu Asp Val Arg
420 425 430

Lys Gln Tyr Lys Arg Asp Ile Gln Asn Ile Asp Ala Leu Leu His Gln
435 440 445

Ser Ile Gly Ser Thr Leu Tyr Asn Lys Ile Tyr Leu Tyr Glu Asn Met
450 455 460

Asn Ile Asn Asn Leu Thr Ala Thr Leu Gly Ala Asp Leu Val Asp Ser
465 470 475 480

Thr Asp Asn Thr Lys Ile Asn Arg Gly Ile Phe Asn Glu Phe Lys Lys
485 490 495

Asn Phe Lys Tyr Ser Ile Ser Ser Asn Tyr Met Ile Val Asp Ile Asn
500 505 510

Glu Arg Pro Ala Leu Asp Asn Glu Arg Leu Lys Trp Arg Ile Gln Leu
515 520 525

Ser Pro Asp Thr Arg Ala Gly Tyr Leu Glu Asn Gly Lys Leu Ile Leu
530 535 540

Gln Arg Asn Ile Gly Leu Glu Ile Lys Asp Val Gln Ile Ile Lys Gln

545 550 555 560

Ser Glu Lys Glu Tyr Ile Arg Ile Asp Ala Lys Val Val
565 570

<210> 15

<211> 753

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic coding region for Human TPA/B. anthracis
antigen fusion protein

<220>

<221> CDS

<222> (13) .. (744)

<223>

<400> 15

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ctg tgt gga gca gtc ttc gtt tgc ccc agc gcc ggc ggg cat ggg gac	99
Leu Cys Gly Ala Val Phe Val Ser Pro Ser Ala Gly Gly His Gly Asp	
15 20 25	
ggt ggc atg cat gtg aaa gaa aag gag aaa aac aag gac gaa aac aag	147
Val Gly Met His Val Lys Glu Lys Glu Lys Asn Lys Asp Glu Asn Lys	
30 35 40 45	
cgt aaa gac gaa gaa cgt aat aaa aca cag gag gaa cac tta aag gag	195
Arg Lys Asp Glu Glu Arg Asn Lys Thr Gln Glu Glu His Leu Lys Glu	
50 55 60	
atc atg aag cac ata gta aag att gag gta aaa ggc gaa gag gct gta	243
Ile Met Lys His Ile Val Lys Ile Glu Val Lys Gly Glu Glu Ala Val	
65 70 75	
aag aag gag gca gca gaa aaa ctg ttg gag aag gtg cct tct gac gtc	291
Lys Lys Glu Ala Ala Glu Lys Leu Leu Glu Lys Val Pro Ser Asp Val	
80 85 90	
tta gag atg tat aag gcc atc ggc ggt aag atc tat atc gtg gac gga	339
Leu Glu Met Tyr Lys Ala Ile Gly Gly Lys Ile Tyr Ile Val Asp Gly	
95 100 105	
gac atc act aaa cac ata tct ctc gaa gct ctc tcc gag gac aag aaa	387

Asp	Ile	Thr	Lys	His	Ile	Ser	Leu	Glu	Ala	Leu	Ser	Glu	Asp	Lys	Lys	
110					115					120					125	
aag	att	aaa	gac	atc	tac	ggg	aag	gat	gcc	tta	ttg	cac	gag	cac	tac	435
Lys	Ile	Lys	Asp	Ile	Tyr	Gly	Lys	Asp	Ala	Leu	Leu	His	Glu	His	Tyr	
				130					135					140		
gtt	tac	gca	aag	gag	ggc	tat	gag	ccc	gtg	ctc	gtt	att	cag	agt	agt	483
Val	Tyr	Ala	Lys	Glu	Gly	Tyr	Glu	Pro	Val	Leu	Val	Ile	Gln	Ser	Ser	
			145					150					155			
gag	gac	tac	gtc	gag	aat	acc	gag	aaa	gct	ctg	aat	gtg	tat	tac	gag	531
Glu	Asp	Tyr	Val	Glu	Asn	Thr	Glu	Lys	Ala	Leu	Asn	Val	Tyr	Tyr	Glu	
		160					165					170				
atc	gga	aag	att	ctg	tcc	cgg	gac	atc	ctg	tcc	aaa	atc	aac	cag	cca	579
Ile	Gly	Lys	Ile	Leu	Ser	Arg	Asp	Ile	Leu	Ser	Lys	Ile	Asn	Gln	Pro	
	175					180					185					
tac	cag	aaa	ttc	ctt	gat	gtt	ctt	aac	aca	atc	aaa	aac	gcg	tca	gat	627
Tyr	Gln	Lys	Phe	Leu	Asp	Val	Leu	Asn	Thr	Ile	Lys	Asn	Ala	Ser	Asp	
190					195					200					205	
agc	gac	ggg	cag	gat	ctt	ctg	ttt	aca	aat	caa	ctc	aag	gaa	cac	ccc	675
Ser	Asp	Gly	Gln	Asp	Leu	Leu	Phe	Thr	Asn	Gln	Leu	Lys	Glu	His	Pro	
				210					215					220		
act	gat	ttc	agc	gtg	gag	ttc	ctc	gag	cag	aat	tct	aac	gaa	gtc	cag	723
Thr	Asp	Phe	Ser	Val	Glu	Phe	Leu	Glu	Gln	Asn	Ser	Asn	Glu	Val	Gln	
			225					230					235			
gag	gtg	ttc	gcc	aag	gca	ttt	tgaggatcc									753
Glu	Val	Phe	Ala	Lys	Ala	Phe										
		240														

<210> 16

<211> 244

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TPA/B. anthracis antigen fusion protein

<400> 16

Met	Asp	Ala	Met	Lys	Arg	Gly	Leu	Cys	Cys	Val	Leu	Leu	Leu	Cys	Gly
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Ala	Val	Phe	Val	Ser	Pro	Ser	Ala	Gly	Gly	His	Gly	Asp	Val	Gly	Met
			20					25					30		

His	Val	Lys	Glu	Lys	Glu	Lys	Asn	Lys	Asp	Glu	Asn	Lys	Arg	Lys	Asp
		35					40					45			

Glu Glu Arg Asn Lys Thr Gln Glu Glu His Leu Lys Glu Ile Met Lys
50 55 60

His Ile Val Lys Ile Glu Val Lys Gly Glu Glu Ala Val Lys Lys Glu
65 70 75 80

Ala Ala Glu Lys Leu Leu Glu Lys Val Pro Ser Asp Val Leu Glu Met
85 90 95

Tyr Lys Ala Ile Gly Gly Lys Ile Tyr Ile Val Asp Gly Asp Ile Thr
100 105 110

Lys His Ile Ser Leu Glu Ala Leu Ser Glu Asp Lys Lys Lys Ile Lys
115 120 125

Asp Ile Tyr Gly Lys Asp Ala Leu Leu His Glu His Tyr Val Tyr Ala
130 135 140

Lys Glu Gly Tyr Glu Pro Val Leu Val Ile Gln Ser Ser Glu Asp Tyr
145 150 155 160

Val Glu Asn Thr Glu Lys Ala Leu Asn Val Tyr Tyr Glu Ile Gly Lys
165 170 175

Ile Leu Ser Arg Asp Ile Leu Ser Lys Ile Asn Gln Pro Tyr Gln Lys
180 185 190

Phe Leu Asp Val Leu Asn Thr Ile Lys Asn Ala Ser Asp Ser Asp Gly
195 200 205

Gln Asp Leu Leu Phe Thr Asn Gln Leu Lys Glu His Pro Thr Asp Phe
210 215 220

Ser Val Glu Phe Leu Glu Gln Asn Ser Asn Glu Val Gln Glu Val Phe
225 230 235 240

Ala Lys Ala Phe

<210> 17

<211> 1788

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic coding region for Human TPA/synthetic antigen fusion protein

<220>

<221> CDS

<222> (13)..(1779)

<223>

<400> 17

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Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu	
1 5 10	
ctg tgt gga gca gtc ttc gtt tcg ccc agc agc gct ggg cca act gtg	99
Leu Cys Gly Ala Val Phe Val Ser Pro Ser Ser Ala Gly Pro Thr Val	
15 20 25	
ccc gac aga gac aat gat gga atc cct gat agt cta gag gtt gag gga	147
Pro Asp Arg Asp Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly	
30 35 40 45	
tac acg gta gat gtc aag aac aaa agg act ttt ctc tcg cct tgg atc	195
Tyr Thr Val Asp Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile	
50 55 60	
tca aat atc cat gag aag aag ggg ctt acc aag tac aag tcc tcc ccc	243
Ser Asn Ile His Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro	
65 70 75	
gag aag tgg tct acc gct tcc gat cca tat agc gat ttc gag aag gtc	291
Glu Lys Trp Ser Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val	
80 85 90	
aca ggc cgg atc gat aaa cag gtg tct cca gag gct aga cac ccc ctg	339
Thr Gly Arg Ile Asp Lys Gln Val Ser Pro Glu Ala Arg His Pro Leu	
95 100 105	
gta gca gcc tac ccg att gta cac gtg gac atg gag aac atc att cta	387
Val Ala Ala Tyr Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu	
110 115 120 125	
agc aaa aac gag gac cag tcc aca caa aac act gac tcc gag acc cgc	435
Ser Lys Asn Glu Asp Gln Ser Thr Gln Asn Thr Asp Ser Glu Thr Arg	
130 135 140	
acc ata tct aaa cag acc agt act tca agg acc cac acc tct gaa gtg	483
Thr Ile Ser Lys Gln Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val	
145 150 155	
cac ggc aat gcg gaa gtc cat gca tcg ttt ttc gat att ggt ggc tcc	531
His Gly Asn Ala Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser	
160 165 170	
gtg tca gcc ggc ttt agc aat agc cag tcc tcg acg gtt gcc att gac	579
Val Ser Ala Gly Phe Ser Asn Ser Gln Ser Ser Thr Val Ala Ile Asp	

175		180		185		
cac tca ctg tca tta gca ggt gag agg act tgg gct gaa act atg ggt	627					
His Ser Leu Ser Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly						
190		195		200		205
ctg aat acc gcc gat acg gcc cgg ctc aac gca aat att cgg tac gtc	675					
Leu Asn Thr Ala Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val		210		215		220
aac aca ggg act gct cct ata tat aac gtg ctg cct acg aca agt ctt	723					
Asn Thr Gly Thr Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu		225		230		235
gtc ctg ggc aaa cag cag acc ctc gca acc att aag gca aag gaa aat	771					
Val Leu Gly Lys Gln Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn		240		245		250
cag ctg agc cag atc ctc gcc cct aac aac tat tat cca tcc aaa aat	819					
Gln Leu Ser Gln Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn		255		260		265
tta gcc ccc ata gcc ctg aac gcc cag gac gac ttt tcc tct acc ccc	867					
Leu Ala Pro Ile Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro		270		275		285
ata act atg aat tac aat cag ttc ctg gag ctg gaa aag acg aag cag	915					
Ile Thr Met Asn Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln		290		295		300
ctg aga cta gac acc gat cag gtg tat gga aac ata gcg aca tat aac	963					
Leu Arg Leu Asp Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn		305		310		315
ttt gag aac ggc cgc gtg cgc gtc gac act ggg tca cag tgg tct gaa	1011					
Phe Glu Asn Gly Arg Val Arg Val Asp Thr Gly Ser Gln Trp Ser Glu		320		325		330
gtt ctg ccg caa att caa gag aca acc gcc aga att atc ttt aat ggg	1059					
Val Leu Pro Gln Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly		335		340		345
aag gac ttg aac ctt gtc gaa cgt aga att gcc gcc gtg cag ccc agt	1107					
Lys Asp Leu Asn Leu Val Glu Arg Arg Ile Ala Ala Val Gln Pro Ser		350		355		365
gat cca ctc gag acg act aaa ccg gat atg aca ctg aaa gag gct ctg	1155					
Asp Pro Leu Glu Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu		370		375		380
aag att gcc ttc gga ttc aac gaa cct aat ggc aat ttg cag tat cag	1203					
Lys Ile Ala Phe Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln		385		390		395
ggg aaa gac atc aca gag ttt gat ttc aat ttc gat cag cag act tcc	1251					
Gly Lys Asp Ile Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser		400		405		410
caa aat atc aaa aat cag ttg gca gag ctg cag gcc acc aat atc tac	1299					
Gln Asn Ile Lys Asn Gln Leu Ala Glu Leu Gln Ala Thr Asn Ile Tyr		415		420		425

acg gtt ctc gat aaa atc aaa ctt aac gcc aag atg aac ata ttg att 1347
 Thr Val Leu Asp Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile
 430 435 440 445

cga gac aaa cgc ttc cac tac gac cgc aac aat ata gcc gta ggc gct 1395
 Arg Asp Lys Arg Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala
 450 455 460

gat gag tct gtc gtc aag gag gct cat agg gaa gtt atc cag agc agt 1443
 Asp Glu Ser Val Val Lys Glu Ala His Arg Glu Val Ile Gln Ser Ser
 465 470 475

act gaa ggg ctg tta ctt aat atc gac aag gac att cgg aag atc ctg 1491
 Thr Glu Gly Leu Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu
 480 485 490

tcc ggg tat atc gtg gag atc gag gat acc gag ggc ctg aag gaa gtc 1539
 Ser Gly Tyr Ile Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val
 495 500 505

att aac gac cgc tat gat atg ctg cag att tcc agc tta cga cag gac 1587
 Ile Asn Asp Arg Tyr Asp Met Leu Gln Ile Ser Ser Leu Arg Gln Asp
 510 515 520 525

ggg aag aca ttt att gac ttt aaa aag tat aac gac aag cta ccc ctg 1635
 Gly Lys Thr Phe Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu
 530 535 540

tac att tcc aac cca aat tac aaa gtt aat gtg tat gct gta acc aag 1683
 Tyr Ile Ser Asn Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys
 545 550 555

gag aac aca atc atc cag cca agc gag aac ggc gat acc agc aca aat 1731
 Glu Asn Thr Ile Ile Gln Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn
 560 565 570

gga atc aaa aag atc ctt ata ttt agt aaa aaa ggc tac gag atc ggt 1779
 Gly Ile Lys Lys Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly
 575 580 585

tgaggatcc 1788

<210> 18

<211> 589

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TPA/synthetic antigen fusion protein

<400> 18

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
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Ala Val Phe Val Ser Pro Ser Ser Ala Gly Pro Thr Val Pro Asp Arg
20 25 30

Asp Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val
35 40 45

Asp Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile
50 55 60

His Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp
65 70 75 80

Ser Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg
85 90 95

Ile Asp Lys Gln Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala
100 105 110

Tyr Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn
115 120 125

Glu Asp Gln Ser Thr Gln Asn Thr Asp Ser Glu Thr Arg Thr Ile Ser
130 135 140

Lys Gln Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His Gly Asn
145 150 155 160

Ala Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val Ser Ala
165 170 175

Gly Phe Ser Asn Ser Gln Ser Ser Thr Val Ala Ile Asp His Ser Leu
180 185 190

Ser Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr
195 200 205

Ala Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly
210 215 220

Thr Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly
225 230 235 240

Lys Gln Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn Gln Leu Ser
245 250 255

Gln Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro
260 265 270

Ile Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met
275 280 285

Asn Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu
290 295 300

Asp Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn
305 310 315 320

Gly Arg Val Arg Val Asp Thr Gly Ser Gln Trp Ser Glu Val Leu Pro
325 330 335

Gln Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu
340 345 350

Asn Leu Val Glu Arg Arg Ile Ala Ala Val Gln Pro Ser Asp Pro Leu
355 360 365

Glu Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala
370 375 380

Phe Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp
385 390 395 400

Ile Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile
405 410 415

Lys Asn Gln Leu Ala Glu Leu Gln Ala Thr Asn Ile Tyr Thr Val Leu
420 425 430

Asp Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys
435 440 445

Arg Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser
450 455 460

Val Val Lys Glu Ala His Arg Glu Val Ile Gln Ser Ser Thr Glu Gly
465 470 475 480

Leu Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr
485 490 495

Ile Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp
500 505 510

Arg Tyr Asp Met Leu Gln Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr

515		520		525
Phe Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser				
530		535		540
Asn Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr				
545		550	555	560
Ile Ile Gln Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys				
	565		570	575
Lys Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly				
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<210> 19

<211> 2418

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic coding region for Human TPA/synthetic antigen fusion protein

<220>

<221> CDS

<222> (13)..(2409)

<223>

<400> 19

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ctg tgt gga gca gtc ttc gtt tgc ccc agc gcc ggc ggg cat ggg gac	99
Leu Cys Gly Ala Val Phe Val Ser Pro Ser Ala Gly Gly His Gly Asp	
15 20 25	
gtt ggc atg cat gtg aaa gaa aag gag aaa aac aag gac gaa aac aag	147
Val Gly Met His Val Lys Glu Lys Glu Lys Asn Lys Asp Glu Asn Lys	
30 35 40 45	
cgt aaa gac gaa gaa cgt cag aaa aca cag gag gaa cac tta aag gag	195
Arg Lys Asp Glu Glu Arg Gln Lys Thr Gln Glu Glu His Leu Lys Glu	
50 55 60	
atc atg aag cac ata gta aag att gag gta aaa ggc gaa gag gct gta	243

Ile	Met	Lys	His	Ile	Val	Lys	Ile	Glu	Val	Lys	Gly	Glu	Glu	Ala	Val		
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aag	aag	gag	gca	gca	gaa	aaa	ctg	tgt	gag	aag	gtg	cct	tct	gac	gtc	291	
Lys	Lys	Glu	Ala	Ala	Glu	Lys	Leu	Leu	Glu	Lys	Val	Pro	Ser	Asp	Val		
		80					85					90					
tta	gag	atg	tat	aag	gcc	atc	ggc	ggc	aag	atc	tat	atc	gtg	gac	gga	339	
Leu	Glu	Met	Tyr	Lys	Ala	Ile	Gly	Gly	Lys	Ile	Tyr	Ile	Val	Asp	Gly		
	95					100					105						
gac	atc	act	aaa	cac	ata	tct	ctc	gaa	gct	ctc	tcc	gag	gac	aag	aaa	387	
Asp	Ile	Thr	Lys	His	Ile	Ser	Leu	Glu	Ala	Leu	Ser	Glu	Asp	Lys	Lys		
110					115					120					125		
aag	att	aaa	gac	atc	tac	ggg	aag	gat	gcc	tta	ttg	cac	gag	cac	tac	435	
Lys	Ile	Lys	Asp	Ile	Tyr	Gly	Lys	Asp	Ala	Leu	Leu	His	Glu	His	Tyr		
				130					135					140			
gtt	tac	gca	aag	gag	ggc	tat	gag	ccc	gtg	ctc	gtt	att	cag	agt	agt	483	
Val	Tyr	Ala	Lys	Glu	Gly	Tyr	Glu	Pro	Val	Leu	Val	Ile	Gln	Ser	Ser		
			145					150					155				
gag	gac	tac	gtc	gag	aat	acc	gag	aaa	gct	ctg	aat	gtg	tat	tac	gag	531	
Glu	Asp	Tyr	Val	Glu	Asn	Thr	Glu	Lys	Ala	Leu	Asn	Val	Tyr	Tyr	Glu		
		160					165					170					
atc	gga	aag	att	ctg	tcc	cgg	gac	atc	ctg	tcc	aaa	atc	aac	cag	cca	579	
Ile	Gly	Lys	Ile	Leu	Ser	Arg	Asp	Ile	Leu	Ser	Lys	Ile	Asn	Gln	Pro		
	175					180					185						
tac	cag	aaa	ttc	ctt	gat	gtt	ctt	aac	aca	atc	aaa	cag	gag	tca	gat	627	
Tyr	Gln	Lys	Phe	Leu	Asp	Val	Leu	Asn	Thr	Ile	Lys	Gln	Ala	Ser	Asp		
190					195					200					205		
agc	gac	ggg	cag	gat	ctt	ctg	ttt	aca	aat	caa	ctc	aag	gaa	cac	ccc	675	
Ser	Asp	Gly	Gln	Asp	Leu	Leu	Phe	Thr	Asn	Gln	Leu	Lys	Glu	His	Pro		
				210					215					220			
act	gat	ttc	agc	gtg	gag	ttc	ctc	gag	cag	aat	tct	aac	gaa	gtc	cag	723	
Thr	Asp	Phe	Ser	Val	Glu	Phe	Leu	Glu	Gln	Asn	Ser	Asn	Glu	Val	Gln		
			225					230					235				
gag	gtg	ttc	gcc	aag	gca	ttt	gag	tac	tat	atc	gaa	ccc	cag	cat	cgc	771	
Glu	Val	Phe	Ala	Lys	Ala	Phe	Ala	Tyr	Tyr	Ile	Glu	Pro	Gln	His	Arg		
		240					245					250					
gat	gtg	ctc	cag	ctg	tac	gcc	ccg	gag	gca	ttt	aac	tac	atg	gac	aaa	819	
Asp	Val	Leu	Gln	Leu	Tyr	Ala	Pro	Glu	Ala	Phe	Asn	Tyr	Met	Asp	Lys		
		255				260					265						
ttc	aat	gaa	cag	gag	att	cag	ctg	tct	ctg	gag	gaa	ctg	aaa	gac	cag	867	
Phe	Asn	Glu	Gln	Glu	Ile	Gln	Leu	Ser	Leu	Glu	Glu	Leu	Lys	Asp	Gln		
270					275					280					285		
agg	atg	ctc	tcc	cgg	tat	gaa	aag	tgg	gaa	aag	atc	aaa	cag	cat	tac	915	
Arg	Met	Leu	Ser	Arg	Tyr	Glu	Lys	Trp	Glu	Lys	Ile	Lys	Gln	His	Tyr		
				290					295					300			
cag	cat	tgg	tcc	gac	tcc	ctg	tca	gaa	gag	ggg	cgc	ggc	ctg	ttg	aaa	963	
Gln	His	Trp	Ser	Asp	Ser	Leu	Ser	Glu	Glu	Gly	Arg	Gly	Leu	Leu	Lys		
			305					310					315				

aag ttg cag att ccc atc gag cct aag aaa gat gat ata ata cac tct Lys Leu Gln Ile Pro Ile Glu Pro Lys Lys Asp Asp Ile Ile His Ser 320 325 330	1011
cta agc cag gag gag aag gaa ctc ctg aag cgg ata caa atc gac tca Leu Ser Gln Glu Glu Lys Glu Leu Leu Lys Arg Ile Gln Ile Asp Ser 335 340 345	1059
tcc gat ttc ctt agc aca gaa gag aag gag ttt cta aaa aaa ctt cag Ser Asp Phe Leu Ser Thr Glu Glu Lys Glu Phe Leu Lys Lys Leu Gln 350 355 360 365	1107
ata gat att aga gat tca ctg agc gag gaa gag aag gag ctg ctc aac Ile Asp Ile Arg Asp Ser Leu Ser Glu Glu Glu Lys Glu Leu Leu Asn 370 375 380	1155
cga att caa gtc gat agt tcg aac ccc ttg tca gaa aaa gag aag gaa Arg Ile Gln Val Asp Ser Ser Asn Pro Leu Ser Glu Lys Glu Lys Glu 385 390 395	1203
ttc ctg aaa aag ttg aag ctc gac atc cag ccg tac gat att aat cag Phe Leu Lys Lys Leu Lys Leu Asp Ile Gln Pro Tyr Asp Ile Asn Gln 400 405 410	1251
cgg cta caa gac acc ggc ggt ctg att gat agc ccc agc atc aac ctt Arg Leu Gln Asp Thr Gly Gly Leu Ile Asp Ser Pro Ser Ile Asn Leu 415 420 425	1299
gac gta cgg aag caa tat aag cgc gac att caa aat atc gac gcc cta Asp Val Arg Lys Gln Tyr Lys Arg Asp Ile Gln Asn Ile Asp Ala Leu 430 435 440 445	1347
tta cat caa tcc ata ggc tcc acg cta tac aat aaa atc tat cta tac Leu His Gln Ser Ile Gly Ser Thr Leu Tyr Asn Lys Ile Tyr Leu Tyr 450 455 460	1395
gaa aac atg aat att aac cag ctc acc gct aca ctg gga gcg gac ctg Glu Asn Met Asn Ile Asn Gln Leu Thr Ala Thr Leu Gly Ala Asp Leu 465 470 475	1443
gtc gat agt aca gac aac aca aag ata aac aga ggt att ttc aac gaa Val Asp Ser Thr Asp Asn Thr Lys Ile Asn Arg Gly Ile Phe Asn Glu 480 485 490	1491
ttc aaa aag aac ttt aag tat tcg atc agc agt aac tat atg att gtt Phe Lys Lys Asn Phe Lys Tyr Ser Ile Ser Ser Asn Tyr Met Ile Val 495 500 505	1539
gac atc aat gaa cgg ccc gca tta gac aat gag agg ttg aag tgg aga Asp Ile Asn Glu Arg Pro Ala Leu Asp Asn Glu Arg Leu Lys Trp Arg 510 515 520 525	1587
att caa ctg agt cct gat act agg gcc ggc tat ctg gag aac ggg aaa Ile Gln Leu Ser Pro Asp Thr Arg Ala Gly Tyr Leu Glu Asn Gly Lys 530 535 540	1635
ctg atc tta cag cga aac atc ggg ctg gag atc aag gat gtg cag att Leu Ile Leu Gln Arg Asn Ile Gly Leu Glu Ile Lys Asp Val Gln Ile 545 550 555	1683
atc aag cag agc gaa aaa gaa tac att cgc atc gac gcc aag gtg gtg Ile Lys Gln Ser Glu Lys Glu Tyr Ile Arg Ile Asp Ala Lys Val Val 560 565 570 575	1731

560	565	570	
cct aag tca aag atc gat acc aag atc cag gaa gct cag ctc aac att Pro Lys Ser Lys Ile Asp Thr Lys Ile Gln Glu Ala Gln Leu Asn Ile 575 580 585			1779
aac cag gag tgg aat aaa gct ctt ggt ctg cca aaa tac acc aaa ctt Asn Gln Glu Trp Asn Lys Ala Leu Gly Leu Pro Lys Tyr Thr Lys Leu 590 595 600 605			1827
atc acc ttt aat gtg cac aac agg tat gcc tct aat atc gtc gag tca Ile Thr Phe Asn Val His Asn Arg Tyr Ala Ser Asn Ile Val Glu Ser 610 615 620			1875
gca tac ctg att ctc aat gaa tgg aag aac aat att cag tct gac ctg Ala Tyr Leu Ile Leu Asn Glu Trp Lys Asn Asn Ile Gln Ser Asp Leu 625 630 635			1923
atc aag aag gtc acg aat tat ctg gtg gac gga aat ggc aga ttc gtg Ile Lys Lys Val Thr Asn Tyr Leu Val Asp Gly Asn Gly Arg Phe Val 640 645 650			1971
ttc acc gac ata act ttg cca aac att gcc gag caa tac act cat cag Phe Thr Asp Ile Thr Leu Pro Asn Ile Ala Glu Gln Tyr Thr His Gln 655 660 665			2019
gat gaa att tac gag caa gtc cac tcc aaa ggt ctg tat gtt cca gag Asp Glu Ile Tyr Glu Gln Val His Ser Lys Gly Leu Tyr Val Pro Glu 670 675 680 685			2067
tca aga tcg att ctg ctc cat ggt cca tcc aaa ggg gtt gag ctt cga Ser Arg Ser Ile Leu Leu His Gly Pro Ser Lys Gly Val Glu Leu Arg 690 695 700			2115
cag gat tct gag gga ttt atc gct gac ttt gga gcc gct gtg gat gac Gln Asp Ser Glu Gly Phe Ile Ala Asp Phe Gly Ala Val Asp Asp 705 710 715			2163
tac gcc gga tac ctg ttg gat aag cag cag tct gat ctc gtg aca aat Tyr Ala Gly Tyr Leu Leu Asp Lys Gln Gln Ser Asp Leu Val Thr Asn 720 725 730			2211
agc aaa aaa ttc ata gat att ttc aag gag gaa ggg agt cag ctg act Ser Lys Lys Phe Ile Asp Ile Phe Lys Glu Glu Gly Ser Gln Leu Thr 735 740 745			2259
tcc tat ggc cgc acg aac gag gct gaa ttt ttt gcg gaa gcc ttt aga Ser Tyr Gly Arg Thr Asn Glu Ala Glu Phe Phe Ala Glu Ala Phe Arg 750 755 760 765			2307
ctt atg cac agc acc gac cat gct gaa agg ttg aag gtg caa aag aat Leu Met His Ser Thr Asp His Ala Glu Arg Leu Lys Val Gln Lys Asn 770 775 780			2355
gcc cct aaa acc ttc cag ttc ata aat gac cag atc aag ttc atc atc Ala Pro Lys Thr Phe Gln Phe Ile Asn Asp Gln Ile Lys Phe Ile Ile 785 790 795			2403
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<210> 20

<211> 799

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TPA/synthetic antigen fusion protein

<400> 20

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20 25 30

His Val Lys Glu Lys Glu Lys Asn Lys Asp Glu Asn Lys Arg Lys Asp
35 40 45

Glu Glu Arg Gln Lys Thr Gln Glu Glu His Leu Lys Glu Ile Met Lys
50 55 60

His Ile Val Lys Ile Glu Val Lys Gly Glu Glu Ala Val Lys Lys Glu
65 70 75 80

Ala Ala Glu Lys Leu Leu Glu Lys Val Pro Ser Asp Val Leu Glu Met
85 90 95

Tyr Lys Ala Ile Gly Gly Lys Ile Tyr Ile Val Asp Gly Asp Ile Thr
100 105 110

Lys His Ile Ser Leu Glu Ala Leu Ser Glu Asp Lys Lys Lys Ile Lys
115 120 125

Asp Ile Tyr Gly Lys Asp Ala Leu Leu His Glu His Tyr Val Tyr Ala
130 135 140

Lys Glu Gly Tyr Glu Pro Val Leu Val Ile Gln Ser Ser Glu Asp Tyr
145 150 155 160

Val Glu Asn Thr Glu Lys Ala Leu Asn Val Tyr Tyr Glu Ile Gly Lys
165 170 175

Ile Leu Ser Arg Asp Ile Leu Ser Lys Ile Asn Gln Pro Tyr Gln Lys
180 185 190

Phe Leu Asp Val Leu Asn Thr Ile Lys Gln Ala Ser Asp Ser Asp Gly
195 200 205

Gln Asp Leu Leu Phe Thr Asn Gln Leu Lys Glu His Pro Thr Asp Phe
210 215 220

Ser Val Glu Phe Leu Glu Gln Asn Ser Asn Glu Val Gln Glu Val Phe
225 230 235 240

Ala Lys Ala Phe Ala Tyr Tyr Ile Glu Pro Gln His Arg Asp Val Leu
245 250 255

Gln Leu Tyr Ala Pro Glu Ala Phe Asn Tyr Met Asp Lys Phe Asn Glu
260 265 270

Gln Glu Ile Gln Leu Ser Leu Glu Glu Leu Lys Asp Gln Arg Met Leu
275 280 285

Ser Arg Tyr Glu Lys Trp Glu Lys Ile Lys Gln His Tyr Gln His Trp
290 295 300

Ser Asp Ser Leu Ser Glu Glu Gly Arg Gly Leu Leu Lys Lys Leu Gln
305 310 315 320

Ile Pro Ile Glu Pro Lys Lys Asp Asp Ile Ile His Ser Leu Ser Gln
325 330 335

Glu Glu Lys Glu Leu Leu Lys Arg Ile Gln Ile Asp Ser Ser Asp Phe
340 345 350

Leu Ser Thr Glu Glu Lys Glu Phe Leu Lys Lys Leu Gln Ile Asp Ile
355 360 365

Arg Asp Ser Leu Ser Glu Glu Glu Lys Glu Leu Leu Asn Arg Ile Gln
370 375 380

Val Asp Ser Ser Asn Pro Leu Ser Glu Lys Glu Lys Glu Phe Leu Lys
385 390 395 400

Lys Leu Lys Leu Asp Ile Gln Pro Tyr Asp Ile Asn Gln Arg Leu Gln
405 410 415

Asp Thr Gly Gly Leu Ile Asp Ser Pro Ser Ile Asn Leu Asp Val Arg
420 425 430

Lys Gln Tyr Lys Arg Asp Ile Gln Asn Ile Asp Ala Leu Leu His Gln

435		440		445
Ser Ile Gly Ser Thr Leu Tyr Asn Lys Ile Tyr Leu Tyr Glu Asn Met				
450		455		460
Asn Ile Asn Gln Leu Thr Ala Thr Leu Gly Ala Asp Leu Val Asp Ser				
465		470		475
Thr Asp Asn Thr Lys Ile Asn Arg Gly Ile Phe Asn Glu Phe Lys Lys				
	485		490	495
Asn Phe Lys Tyr Ser Ile Ser Ser Asn Tyr Met Ile Val Asp Ile Asn				
	500		505	510
Glu Arg Pro Ala Leu Asp Asn Glu Arg Leu Lys Trp Arg Ile Gln Leu				
	515		520	525
Ser Pro Asp Thr Arg Ala Gly Tyr Leu Glu Asn Gly Lys Leu Ile Leu				
	530		535	540
Gln Arg Asn Ile Gly Leu Glu Ile Lys Asp Val Gln Ile Ile Lys Gln				
	545		550	555
Ser Glu Lys Glu Tyr Ile Arg Ile Asp Ala Lys Val Val Pro Lys Ser				
	565		570	575
Lys Ile Asp Thr Lys Ile Gln Glu Ala Gln Leu Asn Ile Asn Gln Glu				
	580		585	590
Trp Asn Lys Ala Leu Gly Leu Pro Lys Tyr Thr Lys Leu Ile Thr Phe				
	595		600	605
Asn Val His Asn Arg Tyr Ala Ser Asn Ile Val Glu Ser Ala Tyr Leu				
	610		615	620
Ile Leu Asn Glu Trp Lys Asn Asn Ile Gln Ser Asp Leu Ile Lys Lys				
	625		630	635
Val Thr Asn Tyr Leu Val Asp Gly Asn Gly Arg Phe Val Phe Thr Asp				
	645		650	655
Ile Thr Leu Pro Asn Ile Ala Glu Gln Tyr Thr His Gln Asp Glu Ile				
	660		665	670
Tyr Glu Gln Val His Ser Lys Gly Leu Tyr Val Pro Glu Ser Arg Ser				
	675		680	685

Ile Leu Leu His Gly Pro Ser Lys Gly Val Glu Leu Arg Gln Asp Ser
690 695 700

Glu Gly Phe Ile Ala Asp Phe Gly Ala Ala Val Asp Asp Tyr Ala Gly
705 710 715 720

Tyr Leu Leu Asp Lys Gln Gln Ser Asp Leu Val Thr Asn Ser Lys Lys
725 730 735

Phe Ile Asp Ile Phe Lys Glu Glu Gly Ser Gln Leu Thr Ser Tyr Gly
740 745 750

Arg Thr Asn Glu Ala Glu Phe Phe Ala Glu Ala Phe Arg Leu Met His
755 760 765

Ser Thr Asp His Ala Glu Arg Leu Lys Val Gln Lys Asn Ala Pro Lys
770 775 780

Thr Phe Gln Phe Ile Asn Asp Gln Ile Lys Phe Ile Ile Asn Ser
785 790 795

<210> 21

<211> 2292

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic coding region

<400> 21

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agcgagagca gcagccaggg cctgctgggc tactacttca gcgacctgaa cttccaggcc	180
cccatggtgg tgaccagcag caccaccggc gacctgagca tccccagcag cgagctggag	240
aacatcccca gcgagaacca gtacttccag agcgccatct ggagcggctt catcaagggtg	300
aagaagagcg acgagtacac cttcgccacc agcgccgaca accacgtgac catgtgggtg	360
gacgaccagg aggtgatcaa caaggccagc aacagcaaca agatcaggct ggagaagggc	420
aggctgtacc agatcaagat ccagtaccag agggagaacc ccaccgagaa gggcctggac	480
ttcaagctgt actggaccga cagccagaac aagaaggagg tgatcagcag cgacaacctg	540
cagctgcccg agctgaagca gaagagcagc aacagcagga agaagaggag caccagcgcc	600

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tacaccgtgg	acgtgaagaa	caagaggacc	ttcctgagcc	cctggatcag	caacatccac	720
gagaagaagg	gcctgaccaa	gtacaagagc	agccccgaga	agtggagcac	cgccagcgac	780
ccctacagcg	acttcgagaa	ggtgaccggc	aggatcgaca	agaacgtgag	ccccgaggcc	840
aggcaccccc	tggtggccgc	ctaccccatc	gtgcacgtgg	acatggagaa	catcatcctg	900
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aacaccagca	ccagcaggac	ccacaccagc	gaggtgcacg	gcaacgccga	ggtgcacgcc	1020
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ctgaacaccg	ccgacaccgc	caggctgaac	gccaacatca	ggtacgtgaa	caccggcacc	1200
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cccagcaaga	acctggcccc	catcgccctg	aacgcccagg	acgacttcag	cagcaccccc	1380
atcaccatga	actacaacca	gttcctggag	ctggagaaga	ccaagcagct	gaggctggac	1440
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ggcaagacct	tcacgactt	caagaagtac	aacgacaagc	tgcccctgta	catcagcaac	2160
cccaactaca	aggtgaacgt	gtacgccgtg	accaaggaga	acaccatcat	caaccccagc	2220
gagaacggcg	acaccagcac	caacggcatc	aagaagatcc	tgatcttcag	caagaagggc	2280
tacgagatcg	gc					2292

<210> 22

<211> 2427

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic coding region

<400> 22

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accctgagcg gccccgtggt catccccctg gtgcagggcg cggcgggcca cggcgacgtg	120
ggcatgcacg tgaaggagaa ggagaagaac aaggacgaga acaagaggaa ggacgaggag	180
aggaacaaga cccaggagga gcacctgaag gagatcatga agcacatcgt gaagatcgag	240
gtgaagggcg aggaggccgt gaagaaggag gccgccgaga agctgctgga gaaggtgccc	300
agcgacgtgc tggagatgta caaggccatc ggcggaaga tctacatcgt ggacggcgac	360
atcaccaagc acatcagcct ggaggccctg agcgaggaca agaagaagat caaggacatc	420
tacggcaagg acgccctgct gcacgagcac tacgtgtacg ccaaggaggg ctacgagccc	480
gtgctggtga tccagagcag cgaggactac gtggagaaca ccgagaaggc cctgaacgtg	540
tactacgaga tcggcaagat cctgagcagg gacatcctga gcaagatcaa ccagccctac	600
cagaagttcc tggacgtgct gaacaccatc aagaacgcc a gcgacagcga cggccaggac	660
ctgctgttca ccaaccagct gaaggagcac cccaccgact tcagcgtgga gttcctggag	720
cagaacagca acgaggtgca ggaggtgttc gccaaaggcct tcgcctacta catcgagccc	780
cagcacaggg acgtgctgca gctgtacgcc cccgaggcct tcaactacat ggacaagttc	840
aacgagcagg agatcaacct gagcctggag gagctgaagg accagaggat gctgagcagg	900
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tacggcagga ccaacgaggg cgagttcttc gccgaggcct tcaggctgat gcacagcacc 2340
gaccacgccg agaggctgaa ggtgcagaag aacgccccca agaccttcca gttcatcaac 2400
gaccagatca agttcatcat caacagc 2427

<210> 23

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic coding region

<400> 23

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accggcaacc tggaagtgat ccaagccgaa gtgaagcaag aaaatcgact tctgaacgag 120
agcgaaagtt catcacaggg tcttctcgga tactacttca gtgacttgaa tttccaagca 180
ccaatggtgg tgactagtag caccaccggc gatttgagca ttcccagctc tgagttggag 240
aacattccca gcgaaaatca gtacttccag tctgctatct ggtccggatt cattaaggtt 300
aaaaagtccg acgaatatac atttgctacc tcggcggata accatgtgac aatgtgggtg 360
gacgaccagg aagtgatcaa caaggcttca aactctaata aaatccggct cgagaagggg 420
aggctctacc agatcaaaat tcagtaccag cgggaaaacc ctacagaaaa aggactcgat 480

ttcaagctgt	actggacaga	tagccaaaac	aagaaagaag	ttatcagctc	agacaatctg	540
cagttacccg	agctcaagca	gaagagttct	aattctagga	agaaaagatc	tacatccgca	600
gggccaaactg	tgcccgacag	agacaatgat	ggaatccctg	atagtctaga	ggttgagggg	660
tacacggtag	atgtcaagaa	caaaaggact	tttctctcgc	cttgatatac	aaatatccat	720
gagaagaagg	ggcttaccaa	gtacaagtcc	tccccgaga	agtggctctac	cgcttccgat	780
ccatatagcg	atttcgagaa	ggtcacaggc	cggatcgata	aaaatgtgtc	tccagaggct	840
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tcgtttttcg	atattggtgg	atccgtgtca	gccggcttta	gcaatagcaa	ctcctcgacg	1080
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ccaaattaca	aagttaatgt	gtatgctgta	accaaggaga	acacaatcat	caatccaagc	2220
gagaacggcg	ataccagcac	aatggaatc	aaaaagatcc	ttatatttag	taaaaaaggc	2280
tacgagatcg	gttga					2295

<210> 24

<211> 2292

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic coding region

<400> 24

atgaaaaaga ggaaggtgct gatccctctc atggccctgt ctaccatcct ggtagtagc	60
acaggggaacc tggagtgat tcaggccgag gttaagcaag agaataggct gctcaacgag	120
tcagaatctt cgtcacaggg attattgggt tactatTTTT cggacctgaa tttccaggcc	180
ccaatggtcg ttacaagctc cacaacaggc gacctgtcta tccccagctc cgaattggag	240
aacatcccta gcgagaacca atactttcaa agcgctatTT ggtaggctt cataaaagtg	300
aagaagtctg acgaatacac gtttgcaaca tctgccgata accacgtcac tatgtgggtc	360
gatgaccagg aagtcacaa caaggctagt aatagcaaca aaatcagact ggagaaaggg	420
agattgtacc agatcaagat ccagtaccaa cgggaaaacc caacagagaa gggcctcgat	480
tttaaactgt attggactga ctctcagaat aagaaggaag tgattagcag cgacaattta	540
caattacccg agttgaaaca gaagagctct aattcaagga aaaagagatc tacctccgcc	600
ggaccaacag ttccagatag ggataatgat ggaatccctg actcactgga ggtcgagggg	660
tacaccgtgg acgtgaaaaa caaacgcact ttctatcac cctggatctc caacattcac	720
gagaagaagg gtctgactaa gtacaaatcc agcccagaga aatggagcac cgcaagtgat	780
ccttatagtg acttcgagaa ggtgacgggc cggatagaca agaacgtatc acccgaagct	840
cgtcatcctc tggtcgccgc ctaccctatt gtgcatgtgg acatggaaaa catcatcctg	900
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aatacatcca cctcacgcac tcataccagc gaagtgcacg gtaacgctga agtgcacgcg	1020
tccttcttcg acatcggcgg gtccgtgtcc gctggatttt ccaactccaa ctcttcgacc	1080
gtagctattg accacagcct gagccttgcc ggagaaagga catgggcgga gactatgggc	1140
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gccctatTTT acaatgtgct cccaaccaca tcactcgtac tgggaaaaaa ccagacccta	1260
gctactatta aagcgaaaga aaatcagttg tcacagatac tggcacccaa caattattat	1320
ccaagcaaaa acctggcacc catcgcactc aatgcgcagg atgactttag tagtacaccc	1380
attacaatga actacaatca gttccttgag ctcgagaaga ccaagcaact gagactcgac	1440

actgaccagg tgtatggtaa tatcgccacc tacaacttcg aaaacggaag ggtgcgggta 1500
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cgagataagc gcttccatta tgatcgaaat aacatcgag ttggcgccga cgaatcagtt 1920
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ggaaagactt tcattgattt caagaaatac aacgataaac tcccgtgtga tatctccaac 2160
ccaaattata aggtgaatgt gtacgctgtc accaaagaga ataccattat taaccgtct 2220
gagaatggcg acacctccac gaatgggata aaaaaaatcc ttatcttcag taaaaaaggc 2280
tacgagatcg gg 2292

<210> 25

<211> 2292

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic coding region

<400> 25

atgaaaaaaaa ggaaggtggt gatccccctt atggcccttt ccaccatctt ggtatcctca 60
accggcaacc tggagggttat tcaagccgaa gtgaagcagg aaaatagact gctgaacgaa 120
tccgaatcta gttctcaggg tctgctgggc tactatttta gcgacctcaa tttccaggca 180
ccaatggtcg tgacttcgag caccacaggc gacttgagca ttccctcttc cgaactcgag 240
aacataccaa gcgagaatca gtatttttcag tccgcaatct ggtcgggttt tatcaaagta 300
aaaaagagcg acgaatacac ttctgctacg tcagccgata atcatgtgac catgtgggtg 360
gatgaccaag aggtcatcaa taaggcgagt aactctaaca agattcgact ggaaaaggga 420
cgctctatc agattaagat tcagtaccag cgtgagaacc cactgaaaa gggctctggac 480

tttaagctgt attggacgga tagtcagaat aaaaaggagg tgatcagttc agacaacttg	540
caattgcctg agctgaaaca gaagtccagc aactctcggg agaagcgcag tactagcgct	600
ggcccaacag tccccgaccg cgacaatgat gggattcccc attctttgga agtggagggg	660
tacacagtgg acgtgaagaa caagagaaca ttcttgagtc catggattag taatatccat	720
gagaaaaaag gtctaaccaa atacaaaagc agcccagaga agtgggtcaac agcatcggat	780
ccttactccg atttcgagaa agttactggc aggattgaca agaacgtatc tccggaggcc	840
aggcatcctc tcgtcgccgc ttaccggatc gtccacgtcg acatggagaa catcatcctg	900
agtaagaatg aggatcaaag cactcagaat actgattccg agacacggac aatcagtaag	960
aatacctcaa cgagcaggac acacacctct gaagttcacg gcaatgccga ggtgcacgct	1020
tcattcttcg atatcggagg atccgtgagc gcgggcttca gcaactctaa ctcttccact	1080
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gccaccatta aggcaaaaga gaatcaactc tcacagatac tggccccaaa caactattac	1320
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atcaccatga attataacca gttcctggaa ctggaaaaaa ctaagcagct ccgcctggac	1440
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gacaaggata ttagaaaaat cctgagcggg tacatcgttg agatcgaaga taccgaggga	2040
cttaaggaag ttataaacga ccgttatgac atgttaaaca tatcaagcct ccggcaggac	2100
ggtaagacat ttatagattt caagaaatac aacgataagc ttctctttta catctcaaat	2160
cccaactata aggtgaatgt ttatgcagta acaaaagaaa atacaattat taatccatcc	2220
gagaacggcg atacatctac taacgggata aaaaaaatcc tcatcttctc caagaaaggc	2280
tacgagatag gg	2292

<210> 26

<211> 2430

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic coding region

<400> 26

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ggcatgcatg	tgaaagaaaa	ggagaaaaac	aaggacgaaa	acaagcgtaa	agacgaagaa	180
cgtaataaaa	cacaggagga	acacttaaag	gagatcatga	agcacatagt	aaagattgag	240
gtaaaaggcg	aagaggctgt	aaagaaggag	gcagcagaaa	aactgttgga	gaagggtgcct	300
tctgacgtct	tagagatgta	taaggccatc	ggcggtaaga	tctatatcgt	ggacggagac	360
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gtgctcgtta	ttcagagtag	tgaggactac	gtcgagaata	ccgagaaagc	tctgaatgtg	540
tattacgaga	tcggaaagat	tctgtcccgg	gatatcctgt	ccaaaatcaa	ccagccatac	600
cagaaattcc	ttgatgttct	taacacaatc	aaaaacgcgt	cagatagcga	cgggcaggat	660
cttctgttta	caaatcaact	caaggaacac	cccactgatt	tcagcgtgga	gttcctcgag	720
cagaattcta	acgaagtcca	ggaggtgttc	gccaaaggcat	ttgcgtacta	tatcgaaccc	780
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gaggggcgcg	gcctgttgaa	aaagttgcag	attcccatcg	agcctaagaa	agatgatata	1020
atacactctc	taagccagga	ggagaaggaa	ctcctgaagc	ggatacaaat	cgactcatcc	1080
gatttcctta	gcacagaaga	gaaggagttt	ctaaaaaac	ttcagataga	tattagagat	1140
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attaatcagc	ggctacaaga	caccggcggt	ctgattgata	gccccagcat	caaccttgac	1320
gtacggaagc	aatataagcg	cgacattcaa	aatatcgacg	ccctattaca	tcaatccata	1380
ggatccacgc	tatacaataa	aatctatcta	tacgaaaaca	tgaatattaa	caatctcacc	1440

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gctacactgg gagcggacct ggtcgatagt acagacaaca caaagataaa cagaggtatt 1500
ttcaacgaat tcaaaaagaa ctttaagtat tcgatcagca gtaactatat gattgttgac 1560
atcaatgaac ggccccgatt agacaatgag aggttgaagt ggagaattca actgagtcct 1620
gatactaggg ccggctatct ggagaacggg aaactgatct tacagcgaaa catcgggctg 1680
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cacaacaggt atgcctctaa tatcgtcgag tcagcatacc tgattctcaa tgaatggaag 1920
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tatggccgca cgaacgaggc tgaatttttt gcggaagcct ttagacttat gcacagcacc 2340
gaccatgctg aaaggttgaa ggtgcaaaag aatgccccta aaaccttcca gttcataaat 2400
gaccagatca agttcatcat caactcttga 2430

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<210> 27

<211> 2427

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic coding region

<400> 27

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aactgtcag gaccagtgtt catacccctt gtccaggggg ccggcgggtca tggcgatgta 120
ggtatgcatg tgaaagagaa ggaaaaaaat aaagacgaga acaagaggaa ggacgaggaa 180
aggaataaga cccaagagga gcacctgaaa gagatcatga agcatattgt gaaaatcgag 240
gtgaaggggg aagaggccgt gaaaaaagaa gcagctgaga agctgctaga gaaagtgcct 300
tctgacgtcc tcgagatgta caaagcaatc ggcggcaaga ttacattgt tgatggtgac 360

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gaccacgcgg aaagactgaa agtgcagaaa aacgccccaa agacattcca gtttattaac 2400
gaccaaataca agttcataat caattcg 2427

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<211> 2427

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<223> Synthetic coding region

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cggaacaaga cccaggagga gcacctgaaa gagatcatga aacacattgt gaaaatcgaa 240
gttaaagggtg aagaggccgt gaagaaggaa gccgcggaga aactgctgga aaagggtcccg 300
tcggacgtac ttgaaatgta caaggcaatt ggtggcaaaa tctacattgt ggacggggac 360
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<211> 26

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<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

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<210> 30

<211> 29

<212> DNA

<213> Artificial Sequence

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<223> Synthetic PCR primer

<400> 30

ccaccaatat ccgatgcatg gacttccgc

29

<210> 31

<211> 28

<212> DNA

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<223> Synthetic PCR primer

<400> 31

cttgaaggat cctcaaccga tctcgtag

28

<210> 32

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Syntheric PCR Primer

<400> 32

ccatgcatcg gatattggtg gctccgtgtc

30

<210> 33

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Synthetic PCR primer

<400> 33

gtggacgacc aggaagtgat c

21

<210> 34

<211> 25

<212> DNA

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<223> Synthetic PCR primer

<400> 34

ggctatctgt ccagtacagc ttgaa

25

<210> 35

<211> 20

<212> DNA

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<223> Synthetic PCR primer

<400> 35

ccgtgctcgt tattcagagt

20

<210> 36

<211> 20

<212> DNA

<213> Artificial Sequence

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<400> 36

ccttctcttc tgtgctaagg

20

<210> 37

<211> 34

<212> DNA

<213> Artificial Sequence

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<223> Synthetic PCR primer

<400> 37

gaacctggat ccctacacca ccttggcgtc gatg

34

<210> 38

<211> 35

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35

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<211> 876

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antigen fusion protein

<220>

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<400> 39

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1 5 10	
ctg tgt gga gca gtc ttc gtt tcg ccc agc gcc ggc ggg cat ggg gac	99
Leu Cys Gly Ala Val Phe Val Ser Pro Ser Ala Gly Gly His Gly Asp	
15 20 25	
gtt ggc atg cat gtg aaa gaa aag gag aaa aac aag gac gaa aac aag	147
Val Gly Met His Val Lys Glu Lys Glu Lys Asn Lys Asp Glu Asn Lys	
30 35 40 45	
cgt aaa gac gaa gaa cgt aat aaa aca cag gag gaa cac tta aag gag	195
Arg Lys Asp Glu Glu Arg Asn Lys Thr Gln Glu Glu His Leu Lys Glu	
50 55 60	
atc atg aag cac ata gta aag att gag gta aaa ggc gaa gag gct gta	243
Ile Met Lys His Ile Val Lys Ile Glu Val Lys Gly Glu Glu Ala Val	
65 70 75	
aag aag gag gca gca gaa aaa ctg ttg gag aag gtg cct tct gac gtc	291
Lys Lys Glu Ala Ala Glu Lys Leu Leu Glu Lys Val Pro Ser Asp Val	
80 85 90	
tta gag atg tat aag gcc atc ggc ggt aag atc tat atc gtg gac gga	339
Leu Glu Met Tyr Lys Ala Ile Gly Gly Lys Ile Tyr Ile Val Asp Gly	
95 100 105	
gac atc act aaa cac ata tct ctc gaa gct ctc tcc gag gac aag aaa	387
Asp Ile Thr Lys His Ile Ser Leu Glu Ala Leu Ser Glu Asp Lys Lys	
110 115 120 125	
aag att aaa gac atc tac ggg aag gat gcc tta ttg cac gag cac tac	435
Lys Ile Lys Asp Ile Tyr Gly Lys Asp Ala Leu Leu His Glu His Tyr	
130 135 140	
gtt tac gca aag gag ggc tat gag ccc gtg ctc gtt att cag agt agt	483
Val Tyr Ala Lys Glu Gly Tyr Glu Pro Val Leu Val Ile Gln Ser Ser	
145 150 155	
gag gac tac gtc gag aat acc gag aaa gct ctg aat gtg tat tac gag	531
Glu Asp Tyr Val Glu Asn Thr Glu Lys Ala Leu Asn Val Tyr Tyr Glu	
160 165 170	
atc gga aag att ctg tcc cgg gac atc ctg tcc aaa atc aac cag cca	579
Ile Gly Lys Ile Leu Ser Arg Asp Ile Leu Ser Lys Ile Asn Gln Pro	
175 180 185	
tac cag aaa ttc ctt gat gtt ctt aac aca atc aaa aac gcg tca gat	627
Tyr Gln Lys Phe Leu Asp Val Leu Asn Thr Ile Lys Asn Ala Ser Asp	
190 195 200 205	
agc gac ggg cag gat ctt ctg ttt aca aat caa ctc aag gaa cac ccc	675
Ser Asp Gly Gln Asp Leu Leu Phe Thr Asn Gln Leu Lys Glu His Pro	
210 215 220	
act gat ttc agc gtg gag ttc ctc gag cag aat tct aac gaa gtc cag	723
Thr Asp Phe Ser Val Glu Phe Leu Glu Gln Asn Ser Asn Glu Val Gln	
225 230 235	
gag gtg ttc gcc aag gca ttt gcg tac tat atc gaa ccc cag cat cgc	771
Glu Val Phe Ala Lys Ala Phe Ala Tyr Tyr Ile Glu Pro Gln His Arg	

240	245	250	
gat gtg ctc cag ctg tac gcc ccg gag gca ttt aac tac atg gac aaa			819
Asp Val Leu Gln Leu Tyr Ala Pro Glu Ala Phe Asn Tyr Met Asp Lys			
255	260	265	
ttc aat gaa cag gag att aat ctg tct ctg gag gaa ctg aaa gac cag			867
Phe Asn Glu Gln Glu Ile Asn Leu Ser Leu Glu Glu Leu Lys Asp Gln			
270	275	280	285
tga ggatcc			876

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20 25 30	
His Val Lys Glu Lys Glu Lys Asn Lys Asp Glu Asn Lys Arg Lys Asp	
35 40 45	
Glu Glu Arg Asn Lys Thr Gln Glu Glu His Leu Lys Glu Ile Met Lys	
50 55 60	
His Ile Val Lys Ile Glu Val Lys Gly Glu Glu Ala Val Lys Lys Glu	
65 70 75 80	
Ala Ala Glu Lys Leu Leu Glu Lys Val Pro Ser Asp Val Leu Glu Met	
85 90 95	
Tyr Lys Ala Ile Gly Gly Lys Ile Tyr Ile Val Asp Gly Asp Ile Thr	
100 105 110	
Lys His Ile Ser Leu Glu Ala Leu Ser Glu Asp Lys Lys Lys Ile Lys	
115 120 125	
Asp Ile Tyr Gly Lys Asp Ala Leu Leu His Glu His Tyr Val Tyr Ala	

130

135

140

Lys Glu Gly Tyr Glu Pro Val Leu Val Ile Gln Ser Ser Glu Asp Tyr
145 150 155 160

Val Glu Asn Thr Glu Lys Ala Leu Asn Val Tyr Tyr Glu Ile Gly Lys
165 170 175

Ile Leu Ser Arg Asp Ile Leu Ser Lys Ile Asn Gln Pro Tyr Gln Lys
180 185 190

Phe Leu Asp Val Leu Asn Thr Ile Lys Asn Ala Ser Asp Ser Asp Gly
195 200 205

Gln Asp Leu Leu Phe Thr Asn Gln Leu Lys Glu His Pro Thr Asp Phe
210 215 220

Ser Val Glu Phe Leu Glu Gln Asn Ser Asn Glu Val Gln Glu Val Phe
225 230 235 240

Ala Lys Ala Phe Ala Tyr Tyr Ile Glu Pro Gln His Arg Asp Val Leu
245 250 255

Gln Leu Tyr Ala Pro Glu Ala Phe Asn Tyr Met Asp Lys Phe Asn Glu
260 265 270

Gln Glu Ile Asn Leu Ser Leu Glu Glu Leu Lys Asp Gln
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<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

<400> 41

ccatacggat cctcactggg ctttcagttc ctcca

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

<400> 42

ctggagacac ctgtttatcg atcc

24

<210> 43

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

<400> 43

ggatcgataa acaggtgtct ccag

24

<210> 44

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

<400> 44

gaagtactgg tctgtttaga tatggt

26

<210> 45

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

<400> 45
accatatcta aacagaccag tacttc

26

<210> 46

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

<400> 46
cgtcgaggac tggctattgc taa

23

<210> 47

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

<400> 47
ttagcaatag ccagtcctcg acg

23

<210> 48

<211> 22

<212> DNA

<213> Artificial Sequence

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gagggctctgc tgtttgccca gg

22

<210> 49

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<400> 49
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22

<210> 50

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<400> 50
cttcagacca ctgtgaccca gtg

23

<210> 51

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<400> 51
cactgggtca cagtgggtctg aag

23

<210> 52

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Synthetic PCR primer

<400> 52

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gcagagctgc aggccaccaa ta

22

<210> 56

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

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cagtactgct ctggataact tccc

24

<210> 57

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

<400> 57
gggaagttat ccagagcagt actg

24

<210> 58

<211> 25

<212> DNA

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aagctggaaa tctgcagcat atcat

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<210> 59

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

<400> 59

atgatatgct gcagatttcc agctt

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acacaatcat ccagccaagc gag

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<210> 62

<211> 24

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<223> Synthetic PCR primer

<400> 62

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<210> 63

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

<400> 63

cgaagaacgt cagaaaacac agga

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<210> 64

<211> 25

<212> DNA

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<223> Synthetic PCR primer

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25

<210> 65

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

<400> 65

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25

<210> 66

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

<400> 66

ccagagacag ctgaatctcc tggt

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<210> 67

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

<400> 67

aacaggagat tcagctgtct ctgg

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<210> 68

<211> 25

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25

<210> 69

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

<400> 69

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25

<210> 70

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

<400> 70

cctcagaatc ctgtcgaagc tca

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<210> 71

<211> 23

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<213> Artificial Sequence

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<223> Synthetic PCR primer

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23

<210> 72

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

<400> 72

gatcagactg ctgcttatcc aaca

24

<210> 73

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

<400> 73

tgttggataa gcagcagtct gatc

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<210> 74

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Synthetic PCR primer

<400> 74

aggaagtcag ctgactccct tcc

23

<210> 75

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<223> Synthetic PCR primer

<400> 75

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23

<210> 76

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PCR primer

<400> 76

gcagatctgg atcctcaaga g

21